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4 protein - protein search, using SW model

Run on: May 20, 2005, 13:22:17 ; Search time 42 Seconds
(without alignments)

1050.419 Million cell updates/sec

Title: US-10-659-549-3

Perfect score: 3043

Sequence: 1 MALLEHMSDPMLIENFNEQ.....GEARSCGSGQGVWSQKWW 591.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

total number of hits satisfying chosen parameters:

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *

5: /cgm2_6/pctodata/1/iaa/PCUS-COMB.pep:*

6: /cgm2_6/pctodata/1/iaa/backfiles1.pep:*

Result No.	Score	Query Match	Length	DB ID	Description
1	3043	100.0	591	4	US-0-643-657-3
2	2610.5	85.8	633	2	US-0-736-770-3
3	1966.5	64.6	605	4	US-0-949-016-8823
4	1958.5	64.4	592	4	US-0-8736-770-6
5	1958.5	64.4	592	4	US-0-9702-705-1809
6	1958.5	64.4	592	4	US-0-736-457-1809
7	1958.5	64.4	592	4	US-0-9643-657-4
8	1958.5	64.4	592	4	US-0-9671-325-1809
9	1897	62.3	591	2	US-0-8736-770-5
10	1897	62.3	591	4	US-0-9643-657-5
11	1881	61.8	608	2	US-0-8736-770-1
12	1832.5	60.2	583	4	US-0-949-016-8267
13	1765.5	58.0	589	4	US-0-9643-657-14
14	1757.5	57.8	591	4	US-0-9643-657-15
15	1459.5	48.0	620	4	US-0-9643-657-13
16	931.5	30.6	573	4	US-0-9643-657-18
17	526	17.3	147	4	US-0-9370-838-99
18	526	17.3	147	4	US-0-9854-13-99
19	509	16.7	159	4	US-0-9370-838-98
20	509	16.7	159	4	US-0-9854-13-98
21	392	12.9	96	4	US-0-9513-939C-5037
22	296	9.7	103	4	US-0-9643-657-16
23	239	7.9	64	4	US-0-9643-657-17
24	203	6.7	57	4	US-0-9221-976-4483
25	197	6.5	573	4	US-0-9270-767-4491
26	154.5	5.1	1427	4	US-0-958-032-1044
27	151	5.0	1180	4	US-0-943-681A-6636

RESULT 1
US-09-643-6

ALIGNMENTS

28	148	4.9	710	4	US-09-107-532A-5067	Sequence 5067 , Ap
29	148	4.9	1288	4	US-09-919-029-209	Sequence 209 , Ap
30	146.5	4.8	1531	4	US-09-418-710-29	Sequence 29 , Ap
31	146.5	4.8	1531	4	US-09-839-479-29	Sequence 29 , Ap
32	145.5	4.8	568	4	US-09-049-016-1-0580	Sequence 1050 , A
33	144	4.7	1857	4	US-09-919-254-91	Sequence 91 , Ap
34	144	4.7	1972	4	US-09-338-09-1084	Sequence 1084 , Ap
35	144	4.7	1984	4	US-09-949-016-7111	Sequence 7111 , Ap
36	144	4.7	1984	4	US-09-949-016-7112	Sequence 7112 , Ap
37	144	4.7	1984	4	US-09-949-016-7113	Sequence 7113 , Ap
38	142	4.7	1972	4	US-08-875-435B-4	Sequence 4 , Appli
39	141.5	4.7	1527	4	US-09-018-710-27	Sequence 27 , Appli
40	141.5	4.7	1527	4	US-09-839-419-27	Sequence 4 , Appli
41	140.5	4.6	897	1	US-08-095-737-4	Sequence 4 , Appli
42	140.5	4.6	897	1	US-08-048-0-145-4	Sequence 4 , Appli
43	140.5	4.6	897	2	US-08-477-389-4	Sequence 4 , Appli
44	140.5	4.6	1540	4	US-09-949-0-16-7037	Sequence 7037 , Ap

ATLANTA, Georgia 30334
TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
ZIP CODE: 94088

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/643,657

SEQUENCE CHARACTERISTICS:
 LENGTH: 633 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE: Consensus
 US-08-736-770-3

Query Match 85.8%; Score 2610.5; DB 2; Length 633;
 Best Local Similarity 94.4%; Pred. No. 4.8e-217;
 Matches 519; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

Query 1 MALETHNSDPMCLENNENQLKVNQEALBILSATQPVVVAIVGLRTGKSYLMNKLQG 60
 Db 1 MALETHNSDPMCLENNENQLKVNQEALBILSATQPVVVAIVGLRTGKSYLMNKLQG 60

Query 61 KNGKFSVASTVOSHITKGWIWCVPHPNWPNHTLVLVLLTEGLDVEKAIDNNDQIFALAL 120
 Db 61 KNGKFSVASTVOSHITKGWIWCVPHPNWPNHTLFC-TPRPRC-KADNKNDQIFALAL 118

Query 121 LSSTFVNTVVKIDQGAIIDLHNVTTELDLIKARNSPDLDREVDPADSASPPFDLVTL 180
 Db 119 LSSTFVNTVVKIDQGAIIDLHNVTTELDLIKARNSPDLDREVDPADSASPPFDLVTL 178

Query 181 RDPCLGLRIDGQVTPDDEYLENSLRPKQSDQRVNFLPRCLQKFPKKCCFIFDLP 240
 Db 179 KDFCLGLIEDGQVTPDDEYLENSLRPKQSDQRVNFLPRCLQKFPKKCCFIFDLP 238

Query 240 AHOKLAQLETLIDDELEPEFYQQVTEFCSYLFSMSMTKLLPGIMYNGSRLLNLVITYV 299
 Db 239 AHOKLAQLETLIDDELEPEFYQQVTEFCSYLFSMSMTKLLPGIMYNGSRLLNLVITYV 298

Query 300 NATSGDLPCTENAVLAQRENSAAVOKATAHYDOOMGQKVYLPMTLQELLIDLHRTSE 359
 Db 299 NATSGDLPCTENAVLAQRENSAAVOKATAHYDOOMGQKVYLPMTLQELLIDLHRTSE 358

Query 360 REALEVMKNSFDVDSFQKELETLDAKNDICRNLLEASDYSQCSALLKDFGPLEEA 419
 Db 359 REALEVMKNSFDVDSFQKELETLDAKNDICRNLLEASDYSQCSALLKDFGPLEEA 418

Query 420 VRQGIYSKPGGHNLFQTEELKAKYVREPRKGIABEVLOQYKLKSKEVSHALQDQA 479
 Db 419 VRQGIYSKPGGHNLFQTEELKAKYVREPRKGIABEVLOQYKLKSKEVSHALQDQA 478

Query 480 LTTEKKKEAQVAEAKAEQRAAORLAATQRNEOMMEROERLHQEVQRMETIAKQNWLAE 539
 Db 479 LTTEKKKEAQVAEAKAEQRAAORLAATQRNEOMMEROERLHQEVQRMETIAKQNWLAE 538

Query 540 QKMQEQQMQ 549
 Db 539 QKMQEQQMQ 548

RESULT 3
 US-09-949-016-8823
 Sequence 8823, Application US/0949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: Bindman, Olga
 APPLICANT: Au-Young, Janice
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastS3Q Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/736,770
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REFERENCE/DOCKET NUMBER: 36 749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:

NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8823
 LENGTH: 605
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-8823

Query Match 64.6%; Score 1966.5; DB 4; Length 605;
 Best Local Similarity 69.7%; Pred. 2.2e-16;
 Matches 389; Conservative 70; Mismatches 88; Indels 11; Gaps 3;

Qy 1 MAEIHMSDPMLCJENFBQLVNEQAELEILSAITOPVWWVAIVGLYRTGKSYLMNKLAG 60
 Db 14 MASEIHMTPGMLCJENFBQLVNEQAELEILSAITOPVWWVAIVGLYRTGKSYLMNKLAG 73

Qy 61 KNKGFSYVASTYQSHTKGIIWCVPHPNPHTLVLIDTEGLGSDVEKAQNNDIQIFALAL 120
 Db 74 KCKGFSLSTVQSHTKGIIWCVPHPKPQHTLVLIDTEGLGSDVEKCDNQNDSWITALV 133

Qy 121 LLSSTPYYNTVNKIDQGIDLHLNVTEDPLIKARNSPD - LDRVEDPADSASFPPDWW 178
 Db 134 LLSSTPYYNTVNKIDQGIDLHLNVTEDPLIKARNSPD - LDRVEDPADSASFPPDWW 193

Qy 179 TURDFCLGULEIDSQLVTPDEYLENSLRPKQSDQRVONENPRLCIOKFFPKKCFIFDL 238
 Db 194 TURDFCLDLEAQGQPLTPDEYLENTSLKKGTSQDTEFNPLRCIRKPPKCKCFVDR 253

Qy 239 PAHKKLAQLETLIDQDDELEPETYQVTEFCSTYFCSYFVSHMTKTPGGMIMVNGSRKNUVITY 298
 Db 254 PVHRRKLAQLEKLQDEEDLPERTVQVADFCSTYFCSYFVSHMTKTPGGMIMVNGSRKNUVITY 313

Qy 299 VNAISSGDLPCENAVLAQRENSANQVAKLAHYDQMGKQVQLPMTETQELLDLHRS 358
 Db 314 VNAISSGDLPCMENAVLAQIENSANQVAKLAHYDQMGKQVQLPMTETQELLDLHRS 373

Qy 359 BREAIEYVMDVPSKFDYDOSPKELLETLDAKONDICKRNLEASSDYCALKIDIFGPLEE 418
 Db 374 BREAIEYVIRSSPKVDHDLFQKELLAQLEKGRDDFCQKQNEASDRSALLQVIFSPLEE 433

Qy 419 AVKOGIYSKPGGHNLFQKTEELKAKYREPRKGIAEEVILQYIKLKSKEVSYSHAILQTDQ 478
 Db 434 EVKAGIYSKPGGYLRFVQLQDPLKCYKEEPRKGIAEEVILQYIKLKSKEVSNTDAILQTDQ 493

Qy 479 ALTETEKKEAQQVAKAEEKAQVAKLAQRENSAVOKAIAHQVQRQ --- MEIAKQ 534
 Db 494 TLTKEKEIEVERVKAESAQSAKMLQEMQRKNEQMEQKERSYQSHLQLTERMENDRV 553

Qy 535 NWLAEQQ --- KMQEQQ 547
 Db 554 QLKEQBERTLALKLQEQ 571

RESULT 4
 US-08-736-770-6
 Sequence 6, Application US/08736770
 Patent No. 581965
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Au-Young, Janice
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

US-09-702-705-1809
 ; Sequence 1809, Application US/09736457
 ; GENERAL INFORMATION:
 ; Patent No. 6509448
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Panger, Gary
 ; APPLICANT: Vedwick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/702-705
 ; CURRENT FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 1833
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 1809
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-702-705-1809

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
 Best Local Similarity 69.4%; Pred. No. 1.e-160;
 Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALETHMSDPMCLIEENFNEQLKVNQEAEILSATTQPVVVAIVGLYRTGKSYLMNKLAG 60
 Db 1 MASETHMTGPMCLIENTGRMANPBAKILSATTQPVVVAIVGLYRTGKSYLMNKLAG 60

Qy 61 KNGKFSVASTVQSHTKGIIWICWVPHPNWPNHTLVLDFEGLGVKEADNKNDIQIFALAL 120
 Db 61 KNGKFSLGSSTVQSHTKGIIWICWVPHPNWPNHTLVLDFEGLGVKEADNKNDIQIFALAL 120

Qy 121 LLSSTEVNTVNKIDQAGIDLHNVTETLDLJKARNSPD -LDRVEDPADSASFFPDLW 178
 Db 121 LLSSTFVNSIGTINQAMDQLYYTETLIRSKSSDENENBEVADFVSEFFPDPDW 180

Qy 179 TLRDFCLGLEIDGQVTPDEYLENSLRKQGSDORVQNFNLPRLCIQKFPKKKCFIFDL 238
 Db 181 TLRDFSLDADGQPLTPBLYLSSLKKGTSQKDEFNLPRLCIRFPPKKCFVDR 240

Qy 239 PAHOKKLAQLETLDLDEPEFVQVTEPQKTFCSYTFSHMTKLGIMVNGSLKLNLYLTY 298
 Db 241 PVHRRKLAQLEKLODEELDEPEFVQVADFCSYTFSNSTKTKLSSGIIQNGPRLESLYTY 300

Qy 299 VNAISSGDLPCTCENAVLAQRENSAAVOKATAHYDQMGOKVOLPMETLQELLDLHRS 358
 Db 301 VNAISSGDLPCMCENAVLAQIAQIENSAAVOKATAHYEQQGOKVQLPTSLOELLDLHRS 360

Qy 359 EREATEFMKNSKFDVQDQFQKELETLDKQNDICKNLLEASDYYCQALLRDIFGPLEE 418
 Db 361 EREATEFVFRSSPFDVQDQFQKELAQFKEKRDFFCKQNEASSDRCGULLQVTFSPPE 420

Qy 419 AVKQGIIYSPGGHNLFIQKTEELAKYTRPRKGIAEVQYKLSKESVSHAILQTDQ 478
 Db 421 EVKQGIIYSPGGYRFLVQLDQKYYBEPRKQIAEBILQTYLKSKESTMTDILQTDQ 480

Qy 479 ALTETEKCKKEAQYKAAEKAQRLAIAORLONEMMOMERELHQEVRO ---MELAQ 534
 Db 481 TLTEKEKEEVERYRAESAQASAKMLQEMNQEMEOKERSYQEHLKQLTKEMDRV 540

Qy 535 NWLAEQQ ----KMOEQQ 547
 Db 541 QLKEQERTALKQE 558

; Sequence 1809, Application US/09736457
 ; GENERAL INFORMATION:
 ; Patent No. 6509448
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Panger, Gary
 ; APPLICANT: Vedwick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/736-457
 ; CURRENT FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 1864
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 1809
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-736-457-1809

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
 Best Local Similarity 69.4%; Pred. No. 1.e-160;
 Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALETHMSDPMCLIEENFNEQLKVNQEAEILSATTQPVVVAIVGLYRTGKSYLMNKLAG 60
 Db 1 MASETHMTGPMCLIENTGRMANPBAKILSATTQPVVVAIVGLYRTGKSYLMNKLAG 60

Qy 61 KNGKFSVASTVQSHTKGIIWICWVPHPNWPNHTLVLDFEGLGVKEADNKNDIQIFALAL 120
 Db 61 KNGKFSLGSSTVQSHTKGIIWICWVPHPNWPNHTLVLDFEGLGVKEADNKNDIQIFALAL 120

Qy 121 LLSSTEVNTVNKIDQAGIDLHNVTETLDLJKARNSPD -LDRVEDPADSASFFPDLW 178
 Db 121 LLSSTFVNSIGTINQAMDQLYYTETLIRSKSSDENENBEVADFVSEFFPDPDW 180

Qy 179 TLRDFCLGLEIDGQVTPDEYLENSLRKQGSDORVQNFNLPRLCIQKFPKKKCFIFDL 238
 Db 181 TLRDFSLDADGQPLTPBLYLSSLKKGTSQKDEFNLPRLCIRFPPKKCFVDR 240

Qy 239 PAHOKKLAQLETLDLDEPEFVQVTEPQKTFCSYTFSHMTKLGIMVNGSLKLNLYLTY 298
 Db 241 PVHRRKLAQLEKLODEELDEPEFVQVADFCSYTFSNSTKTKLSSGIIQNGPRLESLYTY 300

Qy 299 VNAISSGDLPCTCENAVLAQRENSAAVOKATAHYDQMGOKVOLPMETLQELLDLHRS 358
 Db 301 VNAISSGDLPCMCENAVLAQIAQIENSAAVOKATAHYEQQGOKVQLPTSLOELLDLHRS 360

Qy 359 EREATEFMKNSKFDVQDQFQKELETLDKQNDICKNLLEASDYYCQALLRDIFGPLEE 418
 Db 361 EREATEFVFRSSPFDVQDQFQKELAQFKEKRDFFCKQNEASSDRCGULLQVTFSPPE 420

Qy 419 AVKQGIIYSPGGHNLFIQKTEELAKYTRPRKGIAEVQYKLSKESVSHAILQTDQ 478
 Db 421 EVKQGIIYSPGGYRFLVQLDQKYYBEPRKQIAEBILQTYLKSKESTMTDILQTDQ 480

Qy 479 ALTETEKCKKEAQYKAAEKAQRLAIAORLONEMMOMERELHQEVRO ---MELAQ 534
 Db 481 TLTEKEKEEVERYRAESAQASAKMLQEMNQEMEOKERSYQEHLKQLTKEMDRV 540

Qy 535 NWLAEQQ ----KMOEQQ 547
 Db 541 QLKEQERTALKQE 558

Sequence 4, Application US/09643657
Patent No. 664204
GENERAL INFORMATION:
APPLICANT: Diane Pennica
TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,657
FILING DATE: 17-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,089A
FILING DATE: 25-Jan-1998
ATTORNEY/AGENT INFORMATION:
NAME: Habak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE DOCKET NUMBER: P1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 592 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Db	421	EVKAGIYSSKPGGYRIFVQLQDLIKKYYBEPRKIGQAEEILQTYLKSKESTMIDALQTDQ	480
Qy	479	ALTETEKKKEBAQYKAEEKAQAAQRLAIAQRONEQMOERERLHQEQRVRO --- MEIAKQ	534
Db	481	TILTEKEKE1EVERYTAESACASARMLQEMQRKNEOMMEQRERSYDEHLKULTERMENDRV	540
Qy	535	NWLAEQQ --- -KMCQQ 547	
Db	541	QLKREQERTLALKLQEQE 558	
RESULT 8			
	US-09-671-325-1809		
	Sequence 1809, Application US/09671325		
	Patent No. 6667154		
	GENERAL INFORMATION:		
	APPLICANT: Wang, Tongtong		
	Bangur, Chaitanya S.		
	APPLICANT: Lodes, Michael A.		
	APPLICANT: Fanger, Gary		
	APPLICANT: Vedwick, Tom		
	APPLICANT: Carter, Darrick		
	APPLICANT: Rettner, Marc		
	APPLICANT: Par, Ligun		
	APPLICANT: Mannion, Jane		
	APPLICANT: Fan, Liqun		
	APPLICANT: Diagnosys of Lung Cancer		
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
	FILE REFERENCE: 210121-478C12		
	CURRENT APPLICATION NUMBER: US/09/671,325		
	CURRENT FILING DATE: 2000-09-26		
	NUMBER OF SEQ ID NOS: 1825		
	SOFTWARE: FastSEQ for Windows Version 3.0		
	SEQ ID NO: 1809		
	LENGTH: 592		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-09-671-325-1809		
Qy	Query Match	64.4%; Score 1958.5; DB 4; Length 592;	
	Best Local Similarity	69.4%; Pred. No. 1..1e-160;	
	Matches 387; Conservative	71; Mismatches 89; Indels 11; Gaps 3;	
Qy	1	MALEIHMSPDMCLIEPNFNEQLKYNQEALIELSALTQPVVVVAIVGLYRTGSKSYLMINKL	60
Db	1	MASSHEMTGPMCLIEPNFNEQLKYNQEALIELSALTQPVVVVAIVGLYRTGSKSYLMINKL	60
Qy	61	KNKGFSVASTVOSTKIGWIWCYHPPNVPNHTLVLDTETGLGDYVKADNKNDIQFALAL	120
Db	61	KKCGFSVLSGTVQSTKIGIWWMCYHPKCCEGHILVLDTETGLGDYVKGDQNDSWFALAV	120
Qy	121	LISSTFVNTVNTKIDQGAIIDLHNTTELTDLKARNSPD - LDREVPADASPPFDLVW	178
Db	121	LISSTFVNTVNTKIDQGAIIDLHNTTELTHRISKSPPDENENEVEDSADFVSPFPDFW	180
Qy	179	TURDFCLGLBIDGQVTPDEYLNLSRPKQGSDORVQNFNLPRLICQKEFPKKCCFIFDL	238
Db	181	TURDFSLDLEADQPLTDEYLTSLKUKGTSOKDETFLNPRLICRKFFPKKCCFVFDR	240
Qy	239	PAPOKKLAQELTLPDDELEPEFVQVTEFCSYIFSHSMTKLPIEGIMYNGSRKLKVLYT	298
Db	241	PVHRKLAQELKQDDEBLFVQVADFCSYIFNSKTKLTSQGQVNGPRLSVLVLYT	300
Qy	299	VNAISGQLPCIENAVLAQRENSAIVQKALAHDOONGQKVLQPMETLQBLDLDLHRTS	358
Db	301	VNAISGQLPCMENAVLAQIENSAIVQKALAHDOONGQKVLQPMETLQBLDLDLHRTS	360
Qy	359	ERAEIYFMNSPKDVSFOKELETLIDAKONDICRKNLASSDYC5A11K01FQPLEE	418
Db	361	ERAEIYF1RSSFDVHLFQKELAQLBKRDFFCQNEASSDRCSQSLQV1FSPBLE	420
Qy	419	AVKQG1SKPGGHNLFIGTEELKAKTYREPRG1QAEVUQRYLKSKEVSHIA1LQTDQ	478

Query Match 62.3%; Score 1897; DB 591; Length 591;
 Best Local Similarity 63.5%; Pred. No. 2, 2e-155;
 Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

Query 1 MALETHMSPDMCILTENFENFOLKVNQEALFILSAITOPVYVVAVGGLYTKSYLMNKLAG 60
 DB 1 MAPEENLPGMSLDNTKGVLVNPEAKLILSAITQPVYVVAVGGLYTKSYLMNKLAG 60

Query 61 KNKGFSVASTVOSHITKGIVIWCVPWNHNTLVLDETEGLGDEVKADMNDIQIFAL 120
 DB 61 KKNGFSLGSVYKVSPTKGIVIWCVPWNHNTLVLDETEGLGDEVKADMNDIQIFAL 120

Query 121 LLSSSTFVNTVVKIDQAGIDLLHNTVTEIDLLKARNSPLDVEDPASASFPFDLWVTL 180
 DB 121 LLSSSTFVNTVVKIDQAGIDLLHNTVTEIDLLKARNSPLDVEDPASASFPFDLWVTL 180

Query Match 62.3%; Score 1897; DB 4; Length 591;

US-09-643-657-5

RESULT 10

US-09-643-657-5

Patent No. 6642024

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Au Young, Jenice

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/736,770

REFERENCE/DOCKET NUMBER: PF-0145 US

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 415-855-0555

FILING DATE: 415-855-4166

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-855-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 829177

US-08-736-770-5

Query Match 62.3%; Score 1897; DB 591; Length 591;
 Best Local Similarity 63.5%; Pred. No. 2, 2e-155;
 Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

Query 1 MALETHMSPDMCILTENFENFOLKVNQEALFILSAITOPVYVVAVGGLYTKSYLMNKLAG 60
 DB 1 MAPEENLPGMSLDNTKGVLVNPEAKLILSAITQPVYVVAVGGLYTKSYLMNKLAG 60

Query 61 KNKGFSVASTVOSHITKGIVIWCVPWNHNTLVLDETEGLGDEVKADMNDIQIFAL 120
 DB 61 KKNGFSLGSVYKVSPTKGIVIWCVPWNHNTLVLDETEGLGDEVKADMNDIQIFAL 120

Query 121 LLSSSTFVNTVVKIDQAGIDLLHNTVTEIDLLKARNSPLDVEDPASASFPFDLWVTL 180
 DB 121 LLSSSTFVNTVVKIDQAGIDLLHNTVTEIDLLKARNSPLDVEDPASASFPFDLWVTL 180

Query Match 62.3%; Score 1897; DB 4; Length 591;

US-09-643-657-5

Query Match 62.3%; Score 1897; DB 4; Length 591;

Best Local Similarity 63.5%; Pred. No. 2.2e-155; Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

Qy 1 MALETHMSDPMLIENNEQKVNQBALELISAITOPVWVVAIVGLYRTGKSYLANKLAG 60
 Db 1 MAPEINDPGPSLIDNTKQLVNPNEALKILSAITOPVWVVAIVGLYRTGKSYLANKLAG 60

Qy 61 KNKGPFSVASTVOSHTKGWVWICUPHPNPNTLVLIDTEGLGDEKAQNNDIQIPALAL 120
 Db 61 KNQGFSIGSTVKSHTKGWVWICUPHPNPNTLVLIDTEGLGDEKAQNNDIQIPALAL 120

Qy 121 LLSSTFVNTVNTKIDQGAILLHNTELTDLIKARNSPDLDREVADASASFPDLWVTL 180
 Db 121 LLSSTFVNTVNTKIDQGAILLHNTELTDLIKARNSPDLDREVADASASFPDLWVTL 180

Qy 181 RDFCLGIEIDGOLVTPDDEYLENLSRPFPQGSDFORVNQFLPCLQCFKPKKCFEDLPA 240
 Db 181 RDFTLELVDGPITADYLELTSLRKGTDEKSKSNDPCLQCFKPKKCFEDLPA 240

Qy 241 HOKKLAQETLPDDELEPEFVQVTEPFCSYLFSHMSNTKTLPGGIMMNGSRLKNUVLTYVN 300
 Db 241 PKCYLAHLEQKKEEELNPDFTEQVAFCSYLFSHMSNTKTLPGGIMMNGSRLKNUVLTYVN 300

Qy 301 AISSGDLPCTENAVLALAQRENSAAVQKAIAHYDQMGKQLPMTLQBEILDLIRTSE 360
 Db 301 AISSGDLPCTENAVLALAQRENSAAVQKAIAHYDQMGKQLPMTLQBEILDLIRTSE 360

Qy 361 EAIEVMRKNPSKDVSDFQKELETLDAKNDICKENLAEASDYSQCSALIDIFGPLEEAV 420
 Db 361 EAIEVMRKNPSKDVSDFQKELETLDAKNDICKENLAEASDYSQCSALIDIFGPLEEAV 420

Qy 421 KOGIYSKPGHHNLFIQTKTEELAKAKYKREPRKGKIQABEVILQYKLKSKESVSHAILQDQL 480
 Db 421 KOGTFSKPGGRLFTQKQELNKYYQVPRKGKIQABEVILQYKLKSKESVSHAILQDQL 480

Qy 481 TETEKKKKAAQVKAEEAKAEQARLAMIQRNQEMQPERLHQEVRO ---METAKQNW 536
 Db 481 SEKEKAIEVERIKAAESAEEAKMOLEEQQKQNEEMEQEKEKSQYHQVQLTEKMERDRAQL 540

Qy 537 LAEQQ ---KMQBOOMQVQFNCFCISPLPVTMRCVSGKEEAAARSCGSQOGW 585
 Db 541 MAEQKETLALKQEQE ---RLKEGFENESKR ---LQDIIW 575

RESULT 11

US-08-736-770-1 Sequence 1, Application US/08736770

Patent No. 5811965 GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Au-Young, Jennifer L.
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 COUNTRY: US
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/736,770
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

RESULT 12

US-09-949-016-8267 Sequence 8267, Application US/0949016

Patent No. 6812339 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8267
 LENGTH: 583
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-8267

Query Match 60.2%; Score 1932.5; DB 4; Length 583;
 Best Local Similarity 66.2%; Pred. No. 8.2e-150;
 Matches 366; Conservative 65; Mismatches 91; Indels 31; Gaps 2;

1 MALEIHMSPDMCHIENFNEQLKVNQEALIELSAITOPVWVAIVGLYRTGKSYLMNKLAG 60
 58 MAPBIHMTPCMCLIENTGELVANPEAKVLSAITQPVWVAIVGLYRTGKSYLMNKLAG 117
 61 KNKGFSVASTVQSHTKGWIWCYVPHPNWPHTLVLLDTEGLGDEVEKAENDKNDIQIFALAL 120
 118 KNKGFSLGSVTKGWIWCYVPHPKPEHTLVLLDTEGLGDKVKGNDQNSWIFTAV 177

US-09-949-016-8267

Query Match 60.2%; Score 1932.5; DB 4; Length 583;
 Best Local Similarity 66.2%; Pred. No. 8.2e-150;
 Matches 366; Conservative 65; Mismatches 91; Indels 31; Gaps 2;

1 MALEIHMSPDMCHIENFNEQLKVNQEALIELSAITOPVWVAIVGLYRTGKSYLMNKLAG 60
 178 LLSSSTLVVNSMGTNQAMDOLQYVTVTTRISKSDDENENEDSAFVS FFPDFWTI 237
 181 RDPFGIGLEIDGQLYTPDPEYLNLSLRPKQGDSQVRQVNENPLRCLQKEFPKRCFIFDIPA 240
 238 RDPFDLDEADGQJLPDPDEYLNLSLRPKQGDSQVRQVNENPLRCLQKEFPKRCFVFDIPA 297
 241 HOKKLAQELTLPDDELPFVQVTEFCFSYIFSHSMTHKTPLGGMIMVNGSRILKMLVITYVN 300
 298 HRRXLAQELQKLDSELPDFVQVQADFCSYIFNSNKTTLSGG1KVNQSPRLESVLVYIN 357

Db 301 AISSGDLPCIEAVLALLAORENSAVQKAIAHYDQMQCKVQLPMEITQELLDLHRSER 360
 358 AISRGDLPCMENAVLALLAORENSAVQKAIAHYDQMQCKVQLPAETQELLDLHRAQ-- 415

Db 361 EAIEVMKNSFKDQDVQDFQSKORELETLDAKQNDICRKRNIAASSDYSCAALKD1FGPLEAV 420
 416 -----LDRKRDDCKQNEASSDRCSSALQVFSPLVEV 450

Db 421 KOGIYSKPGGHNLPQTKTEELKARYTREPRKGIAEETYDQKYLKSKESVSHAIQDQAL 480
 511 TEKEKEIYECVKAESQADQKDLKKEYEPFRKGIAEETDQTYLKSKESTDAIQTQDIL 510

Db 537 LABQQM2EQCMQ 549

Db 571 LBEQEKTTSKQ 583

RESULT 13
 US-09-949-016-8267-14
 Sequence 14, Application US/09643657
 Patent No. 6642024
 GENERAL INFORMATION:
 APPLICANT: Diane Pennica
 TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California

QY 481 TEPEKKKEAQVKAEEKAQRLAIIQRNEQMMQERLHQEQVRO---MEIAKQNW 536
 Db 541 MAEQQRISLKLQOE 556

QY 537 LABQQ----KMQEQQ 547

Db 541 MAEQQRISLKLQOE 556

QY 481 TEKEQIEMERIKAEEAANRALEMOKHMEMEQKEQSYOEHMKOLTERMEQERKEL 540

QY 421 KOGIYSKPGGHNLPQTKTEELKARYTREPRKGIAEETYDQKYLKSKESVSHAIQDQAL 480
 Db 421 KQGTFYKQGGYVLFQRLQKELCKYIQTPGKGHQAEVMLRKYFESKEQDADTLLKMDQSL 480

QY 361 EAIEVMKNSFKDQDVQDFQSKORELETLDAKQNDICRKRNIAASSDYSCAALKD1FGPLEAV 420
 Db 361 EAIEVMKNSFKDQDVQDFQSKORELETLDAKQNDICRKRNIAASSDYSCAALKD1FGPLEAV 420

QY 421 KOGIYSKPGGHNLPQTKTEELKARYTREPRKGIAEETYDQKYLKSKESVSHAIQDQAL 480
 Db 421 KQGTFYKQGGYVLFQRLQKELCKYIQTPGKGHQAEVMLRKYFESKEQDADTLLKMDQSL 480

QY 481 TEPEKKKEAQVKAEEKAQRLAIIQRNEQMMQERLHQEQVRO---MEIAKQNW 536
 Db 481 TEKEQIEMERIKAEEAANRALEMOKHMEMEQKEQSYOEHMKOLTERMEQERKEL 540

RESULT 14
 US-09-643-657-15
 Sequence 15, Application US/09643657
 GENERAL INFORMATION:
 APPLICANT: Diane Pennica
 TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/643,657
 FILING DATE: 17-Aug-2000
 PRIORITY INFORMATION:
 CLASSIFICATION: <Unknown>
 APPLICATION NUMBER: 09/015,089A

ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1996
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 591 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-643-657-15

Query Match 57.8%; Score 1757.5; DB 4; Length 591;
 Best Local Similarity 63.3%; Pred. No. 2.6e-143;
 Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;

Qy 1 MALEIMIDPNCIENFBQLKVNQBALEIISAITOPVYVVAIVGLYRTGSKYLMNKLAG 60
 Db 2 MASEIMHMLQPMCLIENTAEHLVINGEARLILSAINOPVYVVAIVGLYRTGSKYLMNKLAG 62
 Qy 3 KRGFSLGSLSTVQSHTGIVMMICVPHPKKAGTQLVLDTEGLEDVEKGDNQDCWFALAV 122

Qy 61 KNGKPSVASTVQSHTGIVMMICVPHPKKAGTQLVLDTEGLEDVEKGDNQDCWFALAV 120
 Db 63 KRTGFSLGSLSTVQSHTGIVMMICVPHPKKAGTQLVLDTEGLEDVEKGDNQDCWFALAV 122

Qy 121 LLSSTPVVNTVYKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 122 LLSSTPVVNSGTINGQAMDQHYYTELDTIKSKSPDQGIDDSANFVGFEPPTWAL 182

Qy 181 RDFCGLEIDQQLTVDPEYLNLRPKQGSDPORVNFLPRLCIOKPPKKCFIDPLA 240
 Db 183 RDFSBLEVNKGKLTVDPEYLNLRPKQGSDPORVNFLPRLCIRKPKRKCFFDRPA 242

Qy 241 HQKKLAQLETFIDPEFVQQTETFCYFHSNTKLFQGIMVQYFQVPMNPNTLVLQDTEGJDEVKADNDIQFALALLSSTF 300
 Db 243 LRKQCKLKTETGEEELCSEFVQVAFSTSYFISVAKTISLGGIIVNGPRKSLVQTYG 302

Qy 301 AISSGDLPCIEAVALAAQRENSAAYQKATAHYDQMGKQVQPMETLQELDLHRTSER 360
 Db 303 AISSGSLPCIEAVALAAQRENSAAYQKATAHYDQMGKQVQPMETLQELDLHRTSER 362

Qy 361 BAIIEVPMKNSPKDVSFQKRELETLDAKONDICKRNLEASSDYSALLKDIFGPLEEAV 420

Db 363 EAIEIFLKNSPKDDQKFQTELGNLILISKRDAFIKNSDVLIEDIFGPLEEAV 422
 Qy 421 KQGIYSKPGGINFLFQTEELKAKYTRPRKGIAEEVQKYLKSKESVSHAILQTDQAL 480
 Db 423 KQGTFSKPGGYFLFLQMRQELKKQAPGKLEAEAVLKCYFESREDIVETLKLKDQSL 482
 Qy 481 TETEKCKEAOYKABAEEKAQRLIAIQORNEOMOERERLHQEVQRMETAKQNLAEQ 540
 Db 483 TEAAKEFEEVAKATAEEAANRELAEKOEKFBLMMQKEEESTQEVRL--TERKKEEQ 539
 Qy 541 QKMQEQQ 547
 Db 540 KRD1IEEQ 546

RESULT 15
 US-09-643-657-13
 Sequence 13, Application US/09643657
 Patent No. 6642024
 GENERAL INFORMATION:
 APPLICANT: Diane Pennica
 TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/643,657
 FILING DATE: 17-Aug-2000
 PRIORITY INFORMATION:
 CLASSIFICATION: <Unknown>
 APPLICATION NUMBER: 09/015,089A

ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1996
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 591 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-643-657-13

Query Match 48.0%; Score 1459.5; DB 4; Length 620;
 Best Local Similarity 51.2%; Pred. No. 1.6e-117;
 Matches 281; Conservative 118; Mismatches 145; Indels 5; Gaps 2;

Qy 7 MSDPMCLIENFNEQKVNQBALEIISAITOPVYVVAIVGLYRTGSKYLMNKLAGKQKGPS 66
 Db 1 MEAPICLVEVNKGKLTVDPEYLNLRPKQGSDPORVNFLPRLCIRKPKRKCFFDRPA 242

Qy 67 VASTVQSHTGIVMMICVPHPKKAGTQLVLDTEGLEDVEKGDNQDCWFALAVLISSTF 126
 Db 61 LGSTVQSETKGIVMMICVPHPKRKCFFDRPA 242

Qy 127 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 128 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 129 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 130 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 131 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 132 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 133 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 134 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 135 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 136 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 137 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 138 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 139 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 140 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 141 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 142 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 143 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 144 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 145 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 146 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 147 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 148 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 149 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 150 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 151 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 152 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 153 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 154 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 155 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 156 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 157 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 158 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 159 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 160 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 161 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 162 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 163 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 164 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 165 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 166 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 167 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 168 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 169 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 170 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 171 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 172 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 173 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 174 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 175 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 176 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 177 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 178 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 179 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 180 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 181 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 182 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 183 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 184 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 185 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 186 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 187 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 188 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 189 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 190 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 191 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 192 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 193 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 194 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 195 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 196 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 197 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 198 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 199 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 200 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 201 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 202 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 203 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 204 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 205 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 206 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 207 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 208 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 209 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 210 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

Qy 211 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180
 Db 212 VNTYNTKIDQGADILHNTTELQIKARNSPDLDRVEDPADASSEFPDILWTL 180

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 Job time : 44 secs

GenCore version 5.1.6
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protein - Protein search, using BW model
 on: May 20, 2005, 13:29:02 ; Search time 136 Seconds
 (without alignments)
 1453.632 Million cell updates/sec

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 perfect score: 3043
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 total number of hits satisfying chosen parameters: 1434725

minimum DB seq length: 0
 maximum DB seq length: 2000000000
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 Maximum Match 100%
 Listing first 45 summaries

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ACKNOWLEDGMENTS

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2	2815	92.5	586	14	US-10-14-0-808-46	Sequence 46, Appl
3	2815	92.5	586	14	US-10-121-049-46	Sequence 46, Appl
4	2815	92.5	586	14	US-10-123-904-46	Sequence 46, Appl
5	2815	92.5	586	14	US-10-140-470-46	Sequence 46, Appl
6	2815	92.5	586	14	US-10-175-746-46	Sequence 46, Appl
7	2815	92.5	586	14	US-10-176-918-46	Sequence 46, Appl
8	2815	92.5	586	14	US-10-176-921-46	Sequence 46, Appl
9	2815	92.5	586	14	US-10-137-865-46	Sequence 46, Appl
10	2815	92.5	586	14	US-10-140-474-46	Sequence 46, Appl
11	2815	92.5	586	14	US-10-142-431-46	Sequence 46, Appl
12	2815	92.5	586	14	US-10-143-114-46	Sequence 46, Appl
13	2815	92.5	586	14	US-10-142-419-46	Sequence 46, Appl

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Query Match 92.3%; Score 2815; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 8.2e-197;
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 Qy 241 HOKKLAQLETLPDDELEPEFYVQTFCSYIFPSHNTKTLPGGIMVNGSLRKLNVLTYN 300
 Db 241 HOKKLAQLETLPDDELEPEFYVQTFCSYIFPSHNTKTLPGGIMVNGSLRKLNVLTYN 300
 Qy 301 AISSGDLPCIENAVLAQRENSAAQKATAHYDQMGKVLQPMETLQELLDLIRTSE 360
 Db 301 AISSGDLPCIENAVLAQRENSAAQKATAHYDQMGKVLQPMETLQELLDLIRTSE 360
 Qy 361 EAIEVMKNSPKDVSFQKELETLDAKONDICKRNLEASSDYSALKDIFGPLEEAV 420
 Db 361 EAIEVMKNSPKDVSFQKELETLDAKONDICKRNLEASSDYSALKDIFGPLEEAV 420
 Qy 421 KQGIYSKPGGHLFIQTKTEELKAKTYREPRKGIAQEBVQYKLKSKEVSHAILQTDAL 480
 Db 421 KQGIYSKPGGHLFIQTKTEELKAKTYREPRKGIAQEBVQYKLKSKEVSHAILQTDAL 480
 Qy 481 TETEKKKEAQVKAEEKAQRLAIIQRLAIIQRENEOMQERERLHQEQVROMTIAKQNWLAEQ 540
 Db 481 TETEKKKEAQVKAEEKAQRLAIIQRLAIIQRENEOMQERERLHQEQVROMTIAKQNWLAEQ 540
 Qy 541 QRMQEQQM 549
 Db 541 QRMQEQQM 549

APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanaabe, Colin K.
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Zhenin, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

FILE REFERENCE: P330R1C182

CURRENT APPLICATION NUMBER: US/10/140,808

CURRENT FILING DATE: 2002-05-07

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 46

LENGTH: 586

TYPE: PRT

ORGANISM: Homo Sapien

US-10-140-808-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 8.2e-197;
 Matches 549; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MALETHMSDPMLIENFNEQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKLAG 60
 Db 1 MALETHMSDPMLIENFNEQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKLAG 60
 Qy 61 KNKGFSVASTVQSHTKGIVWCPHPNPWNTLVLIDTEGLDVEKAIDNNDIQIFPALAL 120
 Db 61 KNKGFSVASTVQSHTKGIVWCPHPNPWNTLVLIDTEGLDVEKAIDNNDIQIFPALAL 120
 Qy 122 LLSSTPVNTYNIKIDQAGIDLHNNTTELIDLKARNSPDLRVEDPADSASFPDLWWTL 180
 Db 122 LLSSTPVNTYNIKIDQAGIDLHNNTTELIDLKARNSPDLRVEDPADSASFPDLWWTL 180
 Qy 181 RDFCLGIBDGLVTPDDEYLENLSLRPKQGSQRYVNFLPRLCIQKFPRKKCFIFDLPKA 240
 Db 181 RDFCLGIBDGLVTPDDEYLENLSLRPKQGSQRYVNFLPRLCIQKFPRKKCFIFDLPKA 240
 Qy 241 HOKKLAQLETLPDDELEPEFYVQTFCSYIFPSHNTKTLPGGIMVNGSLRKLNVLTYN 300
 Db 241 HOKKLAQLETLPDDELEPEFYVQTFCSYIFPSHNTKTLPGGIMVNGSLRKLNVLTYN 300
 Qy 301 AISSGDLPCIENAVLAQRENSAAQKATAHYDQMGKVLQPMETLQELLDLIRTSE 360
 Db 301 AISSGDLPCIENAVLAQRENSAAQKATAHYDQMGKVLQPMETLQELLDLIRTSE 360
 Qy 361 EAIEVMKNSPKDVSFQKELETLDAKONDICKRNLEASSDYSALKDIFGPLEEAV 420
 Db 361 EAIEVMKNSPKDVSFQKELETLDAKONDICKRNLEASSDYSALKDIFGPLEEAV 420
 Qy 421 KQGIYSKPGGHLFIQTKTEELKAKTYREPRKGIAQEBVQYKLKSKEVSHAILQTDAL 480
 Db 421 KQGIYSKPGGHLFIQTKTEELKAKTYREPRKGIAQEBVQYKLKSKEVSHAILQTDAL 480

RESULT 2
 US-10-140-808-46
 Sequence 46, Application US/10/140808
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen

RESULT 5
US-10-140-470-46
Sequence 46, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 46
LENGTH: 586
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0; Indel 0; Gaps 0;

Qy 421 KOGIYSKGGHNLFIQTEELAKAKYRPRKGIAEEVLQVLYKLSKESVSHAILQTDQAL 480
Db 421 KOGIYSKGGHNLFIQTEELAKAKYRPRKGIAEEVLQVLYKLSKESVSHAILQTDQAL 480
Qy 481 TETEKKEKAQVKAEEAKAEQRLAAQORNEQMMQPERLHQEQVQMEIAKQWNLBQ 540
Db 481 TETEKKEKAQVKAEEAKAEQRLAAQORNEQMMQPERLHQEQVQMEIAKQWNLBQ 540
Qy 541 QRMQEQQMQ 549
Db 541 QRMQEQQMQ 549

RESULT 6
US-10-175-746-46
Sequence 46, Application US/10175746
Publication No. US2003002270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 46
LENGTH: 586
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-746-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0; Indel 0; Gaps 0;

Qy 1 MALEIHMSPMCLIEENFNEQKVNQSALEILSITAOPVWVVAIVGLYRTGSKSYLMNKLAG 60
Db 1 MALEIHMSPMCLIEENFNEQKVNQSALEILSITAOPVWVVAIVGLYRTGSKSYLMNKLAG 60
Qy 61 KNKGFSVASTVQSHTRGWIWCVPHNWPNHTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Db 61 KNKGFSVASTVQSHTRGWIWCVPHNWPNHTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Qy 121 LLSSTPVNTVNKIDOGAIDLHNTTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Db 121 LLSSTPVNTVNKIDOGAIDLHNTTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Qy 181 RDFCLGIEIDSQLVTPDEYLENSLRPKQGSDQRVNFLPRLCIOPFKKKCF+FDLPA 240
Db 181 RDFCLGIEIDSQLVTPDEYLENSLRPKQGSDQRVNFLPRLCIOPFKKKCF+FDLPA 240
Qy 241 HQKKLAQLETLPDDELEPEFYQVQTEFCSYTFSSHNTKTLPGGIMNGSRLNLVLYN 300
Db 241 HQKKLAQLETLPDDELEPEFYQVQTEFCSYTFSSHNTKTLPGGIMNGSRLNLVLYN 300
Qy 301 AISSGDLPCIENAVLALAORENSAAYOKAIAHYDQOMGQKYOLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIENAVLALAORENSAAYOKAIAHYDQOMGQKYOLPMETLQELLDLHRTSER 360
Qy 361 EAIEVFMKNSPKDQDFQKELTELTDAKONDICKRNLEASSDYSCSALLKDIQFPLBEAV 420
Db 361 EAIEVFMKNSPKDQDFQKELTELTDAKONDICKRNLEASSDYSCSALLKDIQFPLBEAV 420
Qy 421 KOGIYSKPGGNLFIQTEELAKAKYRPRKGIAEEVLQVLYKLSKESVSHAILQTDQAL 480
Db 421 KOGIYSKPGGNLFIQTEELAKAKYRPRKGIAEEVLQVLYKLSKESVSHAILQTDQAL 480
Qy 481 TETEKKEKAQVKAEEAKAEQRLAAQORNEQMMQPERLHQEQVQMEIAKQWNLBQ 540
Db 481 TETEKKEKAQVKAEEAKAEQRLAAQORNEQMMQPERLHQEQVQMEIAKQWNLBQ 540
Qy 541 QRMQEQQMQ 549
Db 541 QRMQEQQMQ 549

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0; Indel 0; Gaps 0;

Qy 1 MALEIHMSPMCLIEENFNEQKVNQSALEILSITAOPVWVVAIVGLYRTGSKSYLMNKLAG 60
Db 1 MALEIHMSPMCLIEENFNEQKVNQSALEILSITAOPVWVVAIVGLYRTGSKSYLMNKLAG 60
Qy 61 KNKGFSVASTVQSHTRGWIWCVPHNWPNHTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Db 61 KNKGFSVASTVQSHTRGWIWCVPHNWPNHTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Qy 121 LLSSTPVNTVNKIDOGAIDLHNTTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Db 121 LLSSTPVNTVNKIDOGAIDLHNTTELDLJARKNSPDLDRVEDPASASFFPDIVWTL 180
Qy 181 RDFCLGIEIDSQLVTPDEYLENSLRPKQGSDQRVNFLPRLCIOPFKKKCF+FDLPA 240
Db 181 RDFCLGIEIDSQLVTPDEYLENSLRPKQGSDQRVNFLPRLCIOPFKKKCF+FDLPA 240
Qy 241 HQKKLAQLETLPDDELEPEFYQVQTEFCSYTFSSHNTKTLPGGIMNGSRLNLVLYN 300
Db 241 HQKKLAQLETLPDDELEPEFYQVQTEFCSYTFSSHNTKTLPGGIMNGSRLNLVLYN 300
Qy 181 RDFCLGIEIDSQLVTPDEYLENSLRPKQGSDQRVNFLPRLCIOPFKKKCF+FDLPA 240

RESULT 7
US-10-176-918-46
Sequence 46, Application US/10176918
; General Information:
; Publication No. US20030027275A1
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3310R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 549; Conservative 0; Mismatches 0; Gaps 0;

Db 181 RDECLGLIEDGOLVTPDEYLENSLRPGIMNGSRKLNVLTVN 240
Qy 241 HOKKLAQELTPDDELEBFVQVTEFESYIFSHSMKTLPGIMNGSRKLNVLTVN 300
Db 241 HOKKLAQELTPDDELEBFVQVTEFESYIFSHSMKTLPGIMNGSRKLNVLTVN 300
Qy 301 AISSGDLPCIEVNLALQRENSAAVOKAIAHYDQMGQKVLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEVNLALQRENSAAVOKAIAHYDQMGQKVLPMETLQELLDLHRTSER 360
Qy 361 EALEVFMKNSFDVQDQSSTQKELETLLAKNDICKRNLEASSDYSCSALLKQIFGLEEAV 420
Db 361 EALEVFMKNSFDVQDQSSTQKELETLLAKNDICKRNLEASSDYSCSALLKQIFGLEEAV 420
Qy 421 KOGIYSKEGGHNLFIQKTEELKAKYRPRKGTAEEVTLQKYLKSKEVSHAILQTDQAL 480
Db 421 KOGIYSKEGGHNLFIQKTEELKAKYRPRKGTAEEVTLQKYLKSKEVSHAILQTDQAL 480
Qy 481 TETEKKKEAQAOKAEEKAQRLAA1QRQNEOMM0ERLHQEVQRMETAKQNLAEQ 540
Db 481 TETEKKKEAQAOKAEEKAQRLAA1QRQNEOMM0ERLHQEVQRMETAKQNLAEQ 540
Qy 541 QRKQEQQQ 549
Db 541 QRKQEQQQ 549

RESULT 8
US-10-176-921-46
Sequence 46, Application US/10176921
; General Information:
; Publication No. US20030027276A1
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-19;
Matches 549; Conservative 0; Mismatches 0; Gaps 0;

Db 1 MALETHMSDMCLIEFNQKVNQEALILSATTQPVVVAIVGLYRTGKSYLMNKAG 60
1 MALETHMSDMCLIEFNQKVNQEALILSATTQPVVVAIVGLYRTGKSYLMNKAG 60
Qy 61 KNKGFSVASTVQSHITKGIVWCPHPNWPNTLVLIDTEGIDVKEADNKNDIQIPALAL 120

FILE REFERENCE: P33301C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-140-474-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Gaps 0;
Db 1 MALETHIMSDPMCLIEENEQLKVNQDALEILSATTOPVVVVAIVGlyRTGKSYLMNKL 60
1 MALETHIMSDPMCLIEENEQLKVNQDALEILSATTOPVVVVAIVGlyRTGKSYLMNKL 60

Qy 61 KNKGFSVASTVQSHTKGIWICVPHPNWPNTLVLIDTEGIDGVEKAQNNDIQLFAL 120
61 KNKGFSVASTVQSHTKGIWICVPHPNWPNTLVLIDTEGIDGVEKAQNNDIQLFAL 120

Db 121 LLSSTPYNTVNTKIDGAIDLHNTELDLKARNSPDLDREVPADSSFPDLVWTL 180
121 LLSSTPYNTVNTKIDGAIDLHNTELDLKARNSPDLDREVPADSSFPDLVWTL 180

Qy 181 RDFCFLGLEIDQVLTEDEYLNLSRPKQGSFQRVNFLPRLCIOKFPRKKCF1FDLPA 240
181 RDFCFLGLEIDQVLTEDEYLNLSRPKQGSFQRVNFLPRLCIOKFPRKKCF1FDLPA 240

Db 181 RDKLQALETLPDDELEPEFYQQTFCSYIFSHSNMTKTLPGGIMMNGSRLKVNVLTYVN 300
241 HOKKLQALETLPDDELEPEFYQQTFCSYIFSHSNMTKTLPGGIMMNGSRLKVNVLTYVN 300

Qy 301 AISSGLPC1ENAVLLAQRENSAAVOKAIAHYDQMGQVQLPMTLQELLDLRTSER 360
301 AISSGLPC1ENAVLLAQRENSAAVOKAIAHYDQMGQVQLPMTLQELLDLRTSER 360

Db 361 EAIEVMKNSPKDVSFQKELETLLDAKNDICKNLLEASDYSALLKDIFGPPEAV 420
361 EAIEVMKNSPKDVSFQKELETLLDAKNDICKNLLEASDYSALLKDIFGPPEAV 420

Qy 421 KQGIYSKPGGHNLP1QKTEELKAKYREPRKGIAPEFVQKYLKSKEVSYSHAILQDQAL 480
421 KQGIYSKPGGHNLP1QKTEELKAKYREPRKGIAPEFVQKYLKSKEVSYSHAILQDQAL 480

Db 481 TETEKKEA0VKAEEAKA0RLLA0QRNE0MM0ERLHQEQVTRMEIAKQWLAEQ 540
481 TETEKKEA0VKAEEAKA0RLLA0QRNE0MM0ERLHQEQVTRMEIAKQWLAEQ 540

Qy 541 QRMQEQQM 549
Db 541 QRMQEQQM 549

RESULT 11
US-10-142-431-46
; Sequence 46, Application US/10142431
; GENERAL INFORMATION:
; APPICLANT: Baker, Kevin P.
; APPICLANT: Beresini, Maureen
; APPICLANT: DeForge, Laura
; APPICLANT: Desnoyers, Luc
; APPICLANT: Filvaroff, Ellen
; APPICLANT: Gao, Wei-Qiang
; APPICLANT: Gerritsen, Mary E.
; APPICLANT: Goddard, Audrey
; APPICLANT: Godowski, Paul J.
; APPICLANT: Gurney, Austin L.
; APPICLANT: Sherwood, Steven
; APPICLANT: Stewart, Timothy A.
; APPICLANT: Tumas, Daniel
; APPICLANT: Watanabe, Colin K
; APPICLANT: Wood, William
; APPICLANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P33301C1251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-142-431-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Gaps 0;
Db 1 MALETHIMSDPMCLIEENEQLKVNQDALEILSATTOPVVVVAIVGlyRTGKSYLMNKL 60
1 MALETHIMSDPMCLIEENEQLKVNQDALEILSATTOPVVVVAIVGlyRTGKSYLMNKL 60

Qy 61 KNKGFSVASTVQSHTKGIWICVPHPNWPNTLVLIDTEGIDGVEKAQNNDIQLFAL 120
61 KNKGFSVASTVQSHTKGIWICVPHPNWPNTLVLIDTEGIDGVEKAQNNDIQLFAL 120

Db 121 LLSSTPYNTVNTKIDGAIDLHNTELDLKARNSPDLDREVPADSSFPDLVWTL 180
121 LLSSTPYNTVNTKIDGAIDLHNTELDLKARNSPDLDREVPADSSFPDLVWTL 180

Qy 181 RDFCFLGLEIDQVLTEDEYLNLSRPKQGSFQRVNFLPRLCIOKFPRKKCF1FDLPA 240
181 RDFCFLGLEIDQVLTEDEYLNLSRPKQGSFQRVNFLPRLCIOKFPRKKCF1FDLPA 240

Db 181 RDKLQALETLPDDELEPEFYQQTFCSYIFSHSNMTKTLPGGIMMNGSRLKVNVLTYVN 300
241 HOKKLQALETLPDDELEPEFYQQTFCSYIFSHSNMTKTLPGGIMMNGSRLKVNVLTYVN 300

Qy 301 AISSGLPC1ENAVLLAQRENSAAVOKAIAHYDQMGQVQLPMTLQELLDLRTSER 360
301 AISSGLPC1ENAVLLAQRENSAAVOKAIAHYDQMGQVQLPMTLQELLDLRTSER 360

Db 361 EAIEVMKNSPKDVSFQKELETLLDAKNDICKNLLEASDYSALLKDIFGPPEAV 420
361 EAIEVMKNSPKDVSFQKELETLLDAKNDICKNLLEASDYSALLKDIFGPPEAV 420

Qy 421 KQGIYSKPGGHNLP1QKTEELKAKYREPRKGIAPEFVQKYLKSKEVSYSHAILQDQAL 480
421 KQGIYSKPGGHNLP1QKTEELKAKYREPRKGIAPEFVQKYLKSKEVSYSHAILQDQAL 480

Db 481 TETEKKEA0VKAEEAKA0RLLA0QRNE0MM0ERLHQEQVTRMEIAKQWLAEQ 540
481 TETEKKEA0VKAEEAKA0RLLA0QRNE0MM0ERLHQEQVTRMEIAKQWLAEQ 540

Qy 541 QRMQEQQM 549
Db 541 QRMQEQQM 549

RESULT 12
US-10-143-114-46
; Sequence 46, Application US/10143114
; GENERAL INFORMATION:
; APPICLANT: Baker, Kevin P.
; APPICLANT: Beresini, Maureen
; APPICLANT: DeForge, Laura
; APPICLANT: Desnoyers, Luc
; APPICLANT: Filvaroff, Ellen
; APPICLANT: Gao, Wei-Qiang
; APPICLANT: Gerritsen, Mary E.
; APPICLANT: Goddard, Audrey
; APPICLANT: Godowski, Paul J.
; APPICLANT: Gurney, Austin L.
; APPICLANT: Sherwood, Steven
; APPICLANT: Stewart, Timothy A.
; APPICLANT: Tumas, Daniel
; APPICLANT: Watanabe, Colin K
; APPICLANT: Wood, William
; APPICLANT: Zhang, Zemin

Query Match 92.5%; Score 2815; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 8.2e-197; Mismatches 0; Indels 0; Gaps 0;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIMSDPMCLIEENFNEQLKVNQEALBILSAITOPVVVAIVGLYRTGKSYLANKLAG 60
 Db 1 MALEIMSDPMCLIEENFNEQLKVNQEALBILSAITOPVVVAIVGLYRTGKSYLANKLAG 60

Qy 61 KNGKFSVASTYQSHTKGIWICVPHPMNPNTLVLIDTEGIDVERADKNDIQIFAL 120
 Db 61 KNGKFSVASTYQSHTKGIWICVPHPMNPNTLVLIDTEGIDVERADKNDIQIFAL 120

Qy 121 LLSSTFVNTYKNDQGADILHNVTELDLJKARNSPDLRVEDPADSASFPDLWTL 180
 Db 121 LLSSTFVNTYKNDQGADILHNVTELDLJKARNSPDLRVEDPADSASFPDLWTL 180

Qy 181 RDPCLGLIEDGQLVTDPEYLENSLRPKGQSDORVQNFNLPRLCIQKFPKKCFIFDLP 240
 Db 181 RDPCLGLIEDGQLVTDPEYLENSLRPKGQSDORVQNFNLPRLCIQKFPKKCFIFDLP 240

Qy 241 HOKKLAQLETLPDDELEPEFYQQTFCSYIFSHSMTKLPGGIMVNGSRUKNLVYV 300
 Db 241 HOKKLAQLETLPDDELEPEFYQQTFCSYIFSHSMTKLPGGIMVNGSRUKNLVYV 300

Qy 301 AISSGDLPCIENAVLAQRENSAAVQAKAIHYDOQMGOKVQLPMTLQELLDLHRTSER 360
 Db 301 AISSGDLPCIENAVLAQRENSAAVQAKAIHYDOQMGOKVQLPMTLQELLDLHRTSER 360

Qy 361 EAIEVMKNSFKDVSQFQELETLLDAKNDICRNLEASDYSQCSALLDIFGPLEEAV 420
 Db 361 EAIEVMKNSFKDVSQFQELETLLDAKNDICRNLEASDYSQCSALLDIFGPLEEAV 420

Qy 421 KOGIYSKPGHNLFIQTEELKAKYTRPRKGIQABEVQKLKSKEVSVAILOTDQAL 480
 Db 421 KOGIYSKPGHNLFIQTEELKAKYTRPRKGIQABEVQKLKSKEVSVAILOTDQAL 480

Qy 481 TETEKKKEAQYKAAEKAQRLAAIQRQNEQMMOERLHQEQVROMETAKQNLAEQ 540
 Db 481 TETEKKKEAQYKAAEKAQRLAAIQRQNEQMMOERLHQEQVROMETAKQNLAEQ 540

Qy 541 QMQEQQM 549
 Db 541 QMQEQQM 549

RESULT 13 -
 US-10-143-114-46 , Sequence 46, Application US/10142419

; Publication No. US20030044945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary B.
 ; APPLICANT: Goddard, Audrey A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C244
 ; CURRENT APPLICATION NUMBER: US/10/142,419
 ; CURRENT FILING DATE: 2002-05-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 46
 ; LENGTH: 586
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-143-114-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 8.2e-197; Mismatches 0; Indels 0; Gaps 0;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIMSDPMCLIEENFNEQLKVNQEALBILSAITOPVVVAIVGLYRTGKSYLANKLAG 60
 Db 1 MALEIMSDPMCLIEENFNEQLKVNQEALBILSAITOPVVVAIVGLYRTGKSYLANKLAG 60

Qy 61 KNGKFSVASTYQSHTKGIWICVPHPMNPNTLVLIDTEGIDVERADKNDIQIFAL 120
 Db 61 KNGKFSVASTYQSHTKGIWICVPHPMNPNTLVLIDTEGIDVERADKNDIQIFAL 120

Qy 121 LLSSTFVNTYKNDQGADILHNVTELDLJKARNSPDLRVEDPADSASFPDLWTL 180
 Db 121 LLSSTFVNTYKNDQGADILHNVTELDLJKARNSPDLRVEDPADSASFPDLWTL 180

Qy 181 RDPCLGLIEDGQLVTDPEYLENSLRPKGQSDORVQNFNLPRLCIQKFPKKCFIFDLP 240
 Db 181 RDPCLGLIEDGQLVTDPEYLENSLRPKGQSDORVQNFNLPRLCIQKFPKKCFIFDLP 240

Qy 241 HOKKLAQLETLPDDELEPEFYQQTFCSYIFSHSMTKLPGGIMVNGSRUKNLVYV 300
 Db 241 HOKKLAQLETLPDDELEPEFYQQTFCSYIFSHSMTKLPGGIMVNGSRUKNLVYV 300

Qy 301 AISSGDLPCIENAVLAQRENSAAVQAKAIHYDOQMGOKVQLPMTLQELLDLHRTSER 360
 Db 301 AISSGDLPCIENAVLAQRENSAAVQAKAIHYDOQMGOKVQLPMTLQELLDLHRTSER 360

Qy 361 EAIEVMKNSFKDVSQFQELETLLDAKNDICRNLEASDYSQCSALLDIFGPLEEAV 420
 Db 361 EAIEVMKNSFKDVSQFQELETLLDAKNDICRNLEASDYSQCSALLDIFGPLEEAV 420

Qy 421 KOGIYSKPGHNLFIQTEELKAKYTRPRKGIQABEVQKLKSKEVSVAILOTDQAL 480
 Db 421 KOGIYSKPGHNLFIQTEELKAKYTRPRKGIQABEVQKLKSKEVSVAILOTDQAL 480

Qy 481 TETEKKKEAQYKAAEKAQRLAAIQRQNEQMMOERLHQEQVROMETAKQNLAEQ 540
 Db 481 TETEKKKEAQYKAAEKAQRLAAIQRQNEQMMOERLHQEQVROMETAKQNLAEQ 540

Qy 541 QMQEQQM 549

Db	541	 QRMQEQQM	549	Db	421	KOGIYSKPGGHNLFIQKTEELKAKTYREPRKGIAEVQKYLKSKEVS	SHAILQTDQAL	480				
Db	481	TETEKCKKEAQKAEAKAORLAIAQKNEOMM	QERERLHQEVQRMELAKQNLWAEQ	540	Qy	481	TETEKCKKEAQKAEAKAORLAIAQKNEOMM	QERERLHQEVQRMELAKQNLWAEQ	540			
Db	481	TETEKCKKEAQKAEAKAORLAIAQKNEOMM	QERERLHQEVQRMELAKQNLWAEQ	540	Qy	541	QRMQEQQM	549				
Db	541	QRMQEQQM	549	Db	541	QRMQEQQM	549	Qy				
		RESULT 15										
		US-10-142-423-46										
		; Sequence 46, Application US/10123262										
		; Publication No. US20030049816A1										
		GENERAL INFORMATION:										
		APPLICANT: Baker, Kevin P.										
		APPLICANT: Beresini, Maureen										
		APPLICANT: DeForge, Laura										
		APPLICANT: Desnoyers, Luc										
		APPLICANT: Filvaroff, Ellen										
		APPLICANT: Gao, Wei-Qiang										
		APPLICANT: Gerritsen, Mary E.										
		APPLICANT: Goddard, Audrey										
		APPLICANT: Godowski, Paul J.										
		APPLICANT: Gurney, Austin L.										
		APPLICANT: Sherwood, Steven										
		APPLICANT: Smith, Victoria										
		APPLICANT: Stewart, Timothy A.										
		APPLICANT: Tumas, Daniel										
		APPLICANT: Tumas, Daniel										
		APPLICANT: Watanabe, Colin K.										
		APPLICANT: Wood, William										
		APPLICANT: Wood, William										
		APPLICANT: Zhang, Zemin										
		TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC										
		ACIDS ENCODING THE SAME										
		FILE REFERENCE: P3330R1C38										
		CURRENT APPLICATION NUMBER: US/10/123,262										
		CURRENT FILING DATE: 2002-04-15										
		Prior Application removed - See File Wrapper or Palm										
		NUMBER OF SEQ ID NOS: 550										
		SEQ ID NO 46										
		LENGTH: 586										
		TYPE: PRT										
		ORGANISM: Homo Sapien										
		US-10-123-262-46										
Qy	1	MALEIHMSPMCLLNEFNEQALKYNEQAEABILS	ATQPVVVVAIVGLRTGKSYLMNKLAG	60	Query Match	92.5%	Score 2815;	DB 14;				
Db	1	MALEIHMSPMCLLNEFNEQALKYNEQAEABILS	ATQPVVVVAIVGLRTGKSYLMNKLAG	60	Best Local Similarity	100.0%	Pred. No. 8.2e-197;	Length 586;				
Qy	61	KNKGFSVASTVQSTKIGWIWCYPHPNWPNHTLVL	VLDTPEGLDVERADNKNDIQIFAL	120	Matches 549;	Conservative 0;	Mismatches 0;	Indels 0;				
Db	61	KNKGFSVASTVQSTKIGWIWCYPHPNWPNHTLVL	VLDTPEGLDVERADNKNDIQIFAL	120	Gaps 0;							
Qy	121	LLSSTFVNTVNKIDQGAILLNVTE	TLKARNSDLDRVEDPAAASFPDLWTL	180	Qy	1	MALEIHMSPMCLLNEFNEQALKYNEQAEABILS	ATQPVVVVAIVGLRTGKSYLMNKLAG	60			
Db	121	LLSSTFVNTVNKIDQGAILLNVTE	TLKARNSDLDRVEDPAAASFPDLWTL	180	Db	1	MALEIHMSPMCLLNEFNEQALKYNEQAEABILS	ATQPVVVVAIVGLRTGKSYLMNKLAG	60			
Qy	181	RDFCLGILEIDGQVTPDEYLENSLRPKQGSDQ	VRQVNFLPRLCIQKEPKKCFIFDPA	240	Qy	61	KNKGFSVASTVQSTKIGWIWCYPHPNWPNHTLVL	VLDTPEGLDVERADNKNDIQIFAL	120			
Db	181	RDFCLGILEIDGQVTPDEYLENSLRPKQGSDQ	VRQVNFLPRLCIQKEPKKCFIFDPA	240	Db	61	KNKGFSVASTVQSTKIGWIWCYPHPNWPNHTLVL	VLDTPEGLDVERADNKNDIQIFAL	120			
Qy	241	HOKKLAQLETLPDDELEP	EVQQTEFCSYIFSHSM	MTKLPGGIMVNGSRLKNVLTVN	300	Qy	121	LLSSTFVNTVNKIDQGAILLNVTE	TLKARNSDLDRVEDPAAASFPDLWTL	180		
Db	241	HOKKLAQLETLPDDELEP	EVQQTEFCSYIFSHSM	MTKLPGGIMVNGSRLKNVLTVN	300	Db	121	LLSSTFVNTVNKIDQGAILLNVTE	TLKARNSDLDRVEDPAAASFPDLWTL	180		
Qy	301	AISSGDLPC	TCIENAVLAQRENSAVOKAI	AHYDQMGQKVLPMETIQELLDLHRTSER	360	Qy	181	RDFCLGILEIDGQVTPDEYLENSLRPKQGSDQ	VRQVNFLPRLCIQKEPKKCFIFDPA	240		
Db	301	AISSGDLPC	TCIENAVLAQRENSAVOKAI	AHYDQMGQKVLPMETIQELLDLHRTSER	360	Db	181	RDFCLGILEIDGQVTPDEYLENSLRPKQGSDQ	VRQVNFLPRLCIQKEPKKCFIFDPA	240		
Qy	361	EATEVFMKNSFDQV	DSQKELETLLDAKONDICKRNIEASSD	YQKYLKSKEVS	SHAILQTDQAL	420	Qy	241	HOKKLAQLETLPDDELEP	EVQQTEFCSYIFSHSM	MTKLPGGIMVNGSRLKNVLTVN	300
Db	361	EATEVFMKNSFDQV	DSQKELETLLDAKONDICKRNIEASSD	YQKYLKSKEVS	SHAILQTDQAL	420	Db	241	HOKKLAQLETLPDDELEP	EVQQTEFCSYIFSHSM	MTKLPGGIMVNGSRLKNVLTVN	300
Qy	421	KOGIYSKPGGHNLFQ	TKTKEELKAKTYREPRKGIAEVQ	KYLKSKEVS	SHAILQTDQAL	480	Qy	301	AISSGDLPC	TCIENAVLAQRENSAVOKAI	AHYDQMGQKVLPMETIQELLDLHRTSER	360
Db	421	KOGIYSKPGGHNLFQ	TKTKEELKAKTYREPRKGIAEVQ	KYLKSKEVS	SHAILQTDQAL	480	Db	301	AISSGDLPC	TCIENAVLAQRENSAVOKAI	AHYDQMGQKVLPMETIQELLDLHRTSER	360

Qy 361 EAIIEVMKNSFKDVKDOSFQKELETLLDAKNDICKRNLEASSDYCSCALLKDIFGPLFEAV 420
Db 361 EAIIEVMKNSFKDVKDOSFQKELETLLDAKNDICKRNLEASSDYCSCALLKDIFGPLFEAV 420
Qy 421 KOGIYSKPGHNLFIQKTEELKAKYTRPRGQIAAEVLQKYLKSSESVSAILQTDQAL 480
Db 421 KOGIYSKPGHNLFIQKTEELKAKYTRPRGQIAAEVLQKYLKSSESVSAILQTDQAL 480
Qy 481 TETEKKKKEAQYKAAEAKAAORLAATQRNEQMMOBERLHQEQYTROMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQYKAAEAKAAORLAATQRNEQMMOBERLHQEQYTROMEIAKQNWLAEQ 540
Qy 541 QRMQEQQM Q 549
Db 541 QRMQEQQM Q 549

Search completed: May 20, 2005, 13:44:05
Job time : 138 secs

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Qy	41.9	AVKQGIYSPKGHNLFIQKTEELKAKYREPRKGIAQAEVILQYKLKSKEVSYHAIQDQ	478	Db	301	AISSGDLPCMCENAVLALAQIENSAVEKAIAHYEQQMQRKVQLPTETLQELLDLHRDSER	360
Db	421	EVKAGIYSPKGGLFLFVQLQDIIKKYVEPKGQIAERLILQKESMSDAILQDQ	480	Qy	361	FAIEFVKNSKFQDQFQKELETLLDAKONDICKRNLEASSDYCSALLKDIFGLEEAV	420
Qy	47.9	ALTETEKEKKKEAOKVAEAKAEQRLAAIQRONEQMMOERLILHQEVHQ---METAKQ	534	Db	361	EAIEFVKNSKFQDQFQKELETLLDAKONDICKRNLEASSDYCSALLKDIFGLEEAV	420
Db	481	TLEKEKEKEEVERYKAEASQAQASAKMLOEMQRKNEQMMEEQKERSYQEHILQLTERMDRV	540	Qy	421	KOGIYSPKGHNLFIQKTEELKAKYREPRKGIAQAEVILQYKLKSKEVSYHAIQDQ	480
Qy	535	NMIAEQQ----KMQEQQ	547	Db	421	XQGTFSPKGGLFLFQKTEELKAKYREPRKGIAQAEVILQYKLKSKEVSYHAIQDQ	480
Db	541	QILKEQERTLALKLQEQE	558	Qy	481	TEKEKEKEAOKVAEAKAEQRLAAIQRONEQMMOERLHQEVHQ---MEIAKQNW	536
RESULT 2							
SG0524				Qy	481	SEKEKA-EVERYKAESEAOKMLEEOKNEEMMEKEKSYQEVHKVOLTEKMERDQL	540
guanine nucleotide-binding protein 2 - human							
C.Species: Homo sapiens (man)							
C.Accession: S70524; S70523; B41268							
Submitted to the EMBL Data Library, May 1995							
A.Reference number: S70524							
A.Accession: S70524							
A.Molecule type: mRNA							
A.Residues: 1-591 <SCH>							
A.Cross-references: Uniprot:P32456; EMBL:M55543; NID:9829176; PMID:AAA67323-1; PID:98291							
R.Neun, R.; Richter, M.F.; Staeheli, P.; Schwemmlle, M.							
PBBs Lett. 390, 69-72, 1996							
A.Title: GTase properties of the interferon-induced human guanylate-binding protein 2.							
A.Reference number: S70523; MUID:96314551; PMID:8706832							
A.Accession: S70523							
A.Molecule type: mRNA							
A.Residues: 1-19 <NEU>							
A.Cross-references: EMBL:M55543							
R.Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.							
Mol. Cell. Biol. 11, 4717-4725, 1991							
A.Title: Interferon-induced Guanylate-binding Proteins lack an N(T)KXD consensus motif a							
A.Reference number: A41268; MUID:91342675; PMID:1715024							
A.Accession: B41268							
A.Molecule type: mRNA							
A.Residues: 'Q', 'A', '9-10', 'NEP', '14-591 <CHE>							
A.Cross-references: GB:M55543							
C.Genetics:							
A.Gene: GDB:GPB2							
A.Cross-references: GDB:378363							
C.Superfamily: guanine nucleotide-binding protein 1							
Query Match Score 62.3%; DB 2; Length 591;							
Best Local Similarity 63.5%; Pred. No. 1.9e-97; Mismatches 88; Indels 28; Gaps 4;							
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;							
Qy	1	MALEIHMSPDMCILLENFNEQKQNEAEILSITQHPLVTPYVVAIYGLYRTGSKYLMNKL	60	Query	58.0%	Score 1765.5; DB 2;	Length 589;
Db	1	MAPEINLPPMSLIDNTNQGQLVVNPPEALKILSATQTPYVVAIYGLYRTGSKYLMNKL	60	Best	Local Similarity 61.7%;	Pred. No. 3.4e-90;	
Qy	61	KNKGFPSVASTVQSHTRKGWIWCVBHPNPNTHTVLLDTEGLVDEVERAKNDIQI	120	Matches	343; Conservative 95; Mismatches 109; Indels 9; Gaps 2;		
Db	61	KNKGFPSVASTVQSHTRKGWIWCVBHPNPNTHTVLLDTEGLVDEVERAKNDIQI	120	Qy	1	MALEIHMSPDMCILLENFNEQKQNEAEILSITQHPLVTPYVVAIYGLYRTGSKYLMNKL	60
Qy	61	QDGAIDLLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	120	Db	1	MASEIHMSPDMCILLENFNEQKQNEAEILSITQHPLVTPYVVAIYGLYRTGSKYLMNKL	60
Db	61	QDGAIDLLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	120	Qy	61	KNKGFPSVASTVQSHTRKGWIWCVBHPNPNTHTVLLDTEGLVDEVERAKNDIQI	120
Qy	121	LLSSTFVNTVNKVLDQGAIIDLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	180	Db	61	KNKGFPSVASTVQSHTRKGWIWCVBHPNPNTHTVLLDTEGLVDEVERAKNDIQI	120
Db	121	LLSSTFVNTVNKVLDQGAIIDLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	180	Qy	121	LLSSTFVNTVNKVLDQGAIIDLLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	180
Qy	121	LLSSTFVNTVNKVLDQGAIIDLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	180	Db	121	LLSSTFVNTVNKVLDQGAIIDLLHNVTELTDLKARNSPDLDRTVDEVERAKNDIQI	180
Qy	181	RDFCLGLIEDGQVLPDTEYLNLSRPLKQGSDQRVNQFLPRCTQKPFKKCFIFDLP	240	Qy	181	RDFCLGLIEDGQVLPDTEYLNLSRPLKQGSDQRVNQFLPRCTQKPFKKCFIFDLP	240
Db	181	RDFCLGLIEDGQVLPDTEYLNLSRPLKQGSDQRVNQFLPRCTQKPFKKCFIFDLP	240	Qy	181	RDFCLGLIEDGQVLPDTEYLNLSRPLKQGSDQRVNQFLPRCTQKPFKKCFIFDLP	240
Qy	241	HQKLAQLEPLPDDLEPEVQQVTEFCSYI FSHSMTHLTPGGI MVNGSRLKVLVYVN	300	Db	241	HQKLAQLEPLPDDLEPEVQQVTEFCSYI FSHSMTHLTPGGI MVNGSRLKVLVYVN	300
Db	241	PKKYLAHLRQLKEELNPPFIEVAEFSYI SFLSHNVTLGGI JAVNGPRLESVYVN	300	Qy	241	PKKYLAHLRQLKEELNPPFIEVAEFSYI SFLSHNVTLGGI JAVNGPRLESVYVN	300
Qy	301	AISSGDLPCMCENAVLALAQIENSAVEKAIAHYEQQMQRKVQLPTETLQELLDLHRDSER	360	Db	241	DRQLSKLEWIQDQLNKEFVEQAEFTSYI SFLSHNVTLGGI JAVNGPRLESVYVN	300

RESULT 4		Guanylate binding protein - mouse	
Qy	301 AISSGDLPCLENVALAQQENSAAVQKLAHYDQMGKQVQLPMBTLOPLLDLHRTSER	481 TETEKKKKEAQVKAEEKAQRLAAJQRENEQMMQERERLHQEQVQRMETAKQNLAEQ	540
Db	301 AICSGELPCKMENAVLTLAQIENSAAVQKATYYEQMNQKIHMPTEPLQPLLDLHRTSER	483 TEAAIEVEIRAKAATAAANRELAEKOEKFELNNQQKEESYQEHYRQL--TEKMKKEQ	539
Qy	361 EAIEVMKNSFKDVSDFQKELETLDAKNDICKRNLLASSDYCSALLKDIKGPLEAV	484 QRMQQQ	547
Db	361 EAIEFMKNSFKDVSDFQKELETLDAKNDICKRNLLASSDYCSALLKDIKGPLEAV	540 KKLIEEQ	546
Qy	421 KQGISTSQPKGHHNLFLQKTEELKAKYVREPRKGQIAFEVYQKLAKSKESYSHAILQDQL	RESULT 5	
Db	421 KQGISTSQPKGHHNLFLQKTEELKAKYVREPRKGQIAFEVYQKLAKSKESYSHAILQDQL	I49884	
Qy	481 TETEKKKKEAQVKAEEKAQRLAAJQRENEQMMQERERLHQEQVQRMETAKQNLAEQ	I49884	
Db	481 TEKEOERIERRKAAEAAANRALAAEMQKCHMELMEQKESYQEHMQLTERMEQEREL	536	
Qy	537 LAEQQ----RMQEQQ	547	
Db	541 MAEQRRIISLKLQEQE	556	
RESULT 4		Guanine nucleotide-binding protein 1	
Qy	S44506	Qy	44 9%; Score 1365.5; DB 2; Length 623;
C	hypothetical protein - rat	C	Best Local Similarity 49.3%; Pred. No. 4-5e-68;
C	Rattus norvegicus (Norway rat)	C	Matches 267; Conservative 112; Mismatches 150; Indels 13; Gaps 3;
C	Date: 13-Jan-1995 #text_change 09-Jul-2004	C	Query Match 44 9%; Score 1365.5; DB 2; Length 623;
C	Accession: S43506	Db	Best Local Similarity 49.3%; Pred. No. 4-5e-68;
C	Biochim. Biophys. Acta 1217, 257-265, 1994	Qy	Matches 267; Conservative 112; Mismatches 150; Indels 13; Gaps 3;
C	Biocitome. Molecular cloning and characterization of an isoprenylated 67 kDa protein.	Db	Query Match 44 9%; Score 1365.5; DB 2; Length 623;
C	Accession: S43506	Qy	Best Local Similarity 49.3%; Pred. No. 4-5e-68;
C	Accession: S43506	Db	Matches 267; Conservative 112; Mismatches 150; Indels 13; Gaps 3;
C	Accession: S43506	Qy	10 PMCL1ENFNEQQLKVNQEALBILSALTQPVVVAIVGLYRTGKSYLMNKLAKGKNGFSVAS
C	Accession: S43506	Db	69 8 PICLVENHNEQQLSYNEQATBILDKSQPVVVAIVGWSHTGKSYLMNCLAGQNHYPLGS
C	Accession: S43506	Qy	70 TVQSTKIGIWIWCWHPNPNHILVLDPEGLDYEKDNKNDQIFALALLSSFVDN
C	Accession: S43506	Db	68 TVQSTKIGIWIWCWHPNPNHILVLDPEGLDYEKDNKNDQIFALALLSSFVDN
C	Accession: S43506	Qy	130 TVNKIDQGAIIDLHNTTELTDLKARNSPDLDREVDPADASFFFDLWVTLRDFCIGLEI
C	Accession: S43506	Db	128 SMNTVNHQALEQLVHVTTELIRKSSSPNPHGYNMSTEVSFFDFTWVTRDFLIELKL
C	Accession: S43506	Qy	190 DGQLVTPDSEYLNSLRPKGSDQYQNFNUPLRCILOKEFFPKKKCFIFDLPAHQKLU-AQL
C	Accession: S43506	Db	248 188 NGEDITSDELENAKLKLIPENNNPRAQASNRSARECRRFNRKCVFNEWPTHDIELRKQL
C	Accession: S43506	Qy	249 ETLPDDELEPFDQVTEFCSYIISHSMTKILPQGIMWGSRLKVLVLTNAISGDLP
C	Accession: S43506	Db	308 248 ETISSDQDDETFKESAMAFASYIIFTYAKLKLTREGIKVYTGNGLGLVTTVDALNSGAVP
C	Accession: S43506	Qy	309 CIENVYALAAQRENAAVOKAIAYDQGQKQVLPMTLQELLDLHRTSBERA1BVFMK
C	Accession: S43506	Db	368 308 CILDVVTTAQRENAAVOKAIYDQGQKQVLPMTLQELLDLHRTSBERA1BVFMK
C	Accession: S43506	Qy	369 NSFKEVDQSFQKELLETLLDAKNDICKRNLLASSDYSYCSALLKDIQPFLEAVKQGQIYSKP
C	Accession: S43506	Db	428 368 HSFKEVDQPLKLQVLELLREKNGLLELLKNEBASDRYQCBEDLRLKQDLMNDI--SFPSV
C	Accession: S43506	Qy	429 GGNHLFQKTEELKAKYVREPRKGQIAEVYQKLKSKESVSHAILQDQALTEKKKK
C	Accession: S43506	Db	488 426 GHRLYMDNREKIDYWQYPRKSYKASAEVQNFQSOQIATIESSSLQADTALTQKATA
C	Accession: S43506	Qy	489 EAQYRAAEKAQRLAAJQRENEQMMQERERLHQEQVQRMETAKQNLAEQQRQEQQQM
C	Accession: S43506	Db	548 486 EKHTYKEAAKEKEQDILRQKEROHQEYMEQERKNEKENFQ
C	Accession: S43506	Qy	549 QV 550
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T17320 hypothetical protein DKFZp564J0863.1 - human (Fragment)
 C.Species: Homo sapiens (man)
 C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R.Dueserhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, September 1999
 A.Reference number: Z18727
 A.Accession: T17320
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-555 <SRO>
 A.Cross-references: UNIPROT:Q9UFL1; EMBL:ALL17600
 A.Experimental source: fetal brain; clone DKFZp564J0863
 C.Genetics:
 A.Note: DKFZp564J0863.1

Query Match 8.3%; Score 251.5; DB 2; Length 555;
 Best Local Similarity 24.9%; Pred. No. 1.2e-05;
 Matches 112; Conservative 68; Mismatches 182; Indels 87; Gaps 19;

Qy 2 ALETHMSDP--MCLIENNEQLKVNQEAELEISAITQ-----PVVVAIVLYRIGTGSY 53
 Db 32 AMESSKPGPQVQLVKQDKHQSFLDEKL--ASILQDHIDLDVVVSVAGAFRKGSF 89

Qy 54 LMN-----KLAGKDKR-----GFSAVSTYCSHTKGWIMW---CVPHPNWPN 90
 Db 90 ILDEMILRVLVSYQSCEGHNSNWNLGQPEEPITGFSRGGSPERTGQIWSVFTVEKPGKK 149

Qy 91 HTYLLDTEPGLGDEKAQNNDLQIFALALLSSTFVYNTVNKIDQAGIDLHNVTELT 150
 Db 150 VAVLMDTQGAFD-SOSTVKDCAIAFALSTMTSSVQYTNLSQNOEDQOLQLEFTYGR 208

Qy 151 LKAKRNSPDLDY-EDPADSASFPPLWTLRDFCLGIEIDGOLVTPPEYLNLSRKQG 209
 Db 209 LA-----MDEIFRKP-----FOTLMLFLVDRDSFPEBYSIGLQGMALDKRLQYKEH 255

Qy 210 SDQRVQNFNLNPLRCIQCFFPKCKKCFIPLPAHKQLACOLETLIPLD----DELEPEFYQV 264
 Db 256 QHEIQNY--RRIHHSSTKTLPEGS--VNGSR-----LKNLVLTYNAISSGDLPCIENAVLA 316

Qy 265 TEFCSYIPTSHSMTKTLPEGSIM----VNGSR-----LKNLVLTYNAISSGDLPCIENAVLA 316
 Db 308 QALIPYVNN-----PRLMKEIINGSKVTCRGLLEYFKAVIKIYQEDLPHPKSMQIA 360

Qy 317 LAQRENSAVQKIAHYQOM---GOKVQLMETLGQDLDLHRTSEREAEVFMKN-- 369
 Db 361 TAYANLAAAASAKDIIYNNMEEVCGGKPKYSPDILE--KHCEFKQLALDHFKCTKK 417

Qy 370 -SPXDVDSFQEKELETLDAKONDICKRN 397
 Db 418 MGKXDFSPRYQQELBEEKELYENFCRN 446

RESULT 7
 A84810 Probable Guanylate binding protein [imported] - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 R.Liu, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Eiss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.;
 Nature 402, 761-768, 1999
 A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
 A.Reference number: A84420; MUID:20083487; PMID:1067197
 A.Accession: A84810
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-217 <SRO>
 A.Cross-references: UNIPROT:Q8SS8C8; GB:AE002093; NID:96598487; PIDN:AACT9624.2; GSPDB:GN
 A.Genetics:
 A.Gene: At2g38840

A;Map position: 2
 H86168 Query Match 7.1%; Score 216; DB 2; Length 217;
 Best Local Similarity 40.9%; Pred. No. 3.5e-03;
 Matches 47; Conservative 26; Mismatches 36; Indels 6; Gaps 3;

Qy 20 QLKVNQEAELEISAITQTPVWVVAIVGLYRIGTGSYLNKLAKGN--KGFSVASTVQSHTKG 77
 Db 28 KLOQSLRSGCLESASRITPISAVATGIGYRSGKSFNLQSLSSYEEFGVHMRDRTKG 87

Qy 78 IWIWCVP--HPNWNHTLVLDTEGLGDEKAQNNDLQIFALALLSSTFVYNTVNK 129
 Db 88 IWWGTPPLEIDGVKTSVIVDTEGFESVGKS-INVYDTRIFALATWSSVLYN 141

RESULT 8
 H86168 Query Match 7.0%; Score 213.5; DB 2; Length 991;
 Best Local Similarity 18.2%; Pred. No. 0.00032;
 Matches 124; Conservative 133; Mismatches 230; Indels 193; Gaps 261;

Qy 18 NEQKLYKVNQEAELEISAITQTPVWVVAIVGLYRIGTGSYLNKLAKGNKGFSVASTVQSHTKG 77
 Db 20 NGRLKTDEAIGALQKLGPGVAVVSLGKALOKSFSIWNQLLSRSIGFEVQTLHRPCNGD 79

Qy 78 IWIWCVP--HPNWNHTLVLDTEGLGDEKAQNNDLQIFALALLSSTFVYNTVNK 133
 Db 80 INWWIEPVKRISEBDGTEYVILWDE---LEDAKS1PTGLGNDIAL-----122
 Qy 134 IDQGAIIDLHNVTELDLKARNSPDLDREVEDPA--DSSAFPDLYVTLRDFGLGLDG 191
 Db 123 -----DLSRLEIRKQDHGEAKDNTFFLGQFSMFMVQLMMDDINSETVEGG 169

Qy 192 QLYTPD-----EYELNSLRPKQGSD-----QRYONF 217
 Db 170 EDYVQNSKLKURPRLLYGVDAIMKFYSERVPKQRGDTIVGPPLAGFTKAFSENVNN 229

Qy 218 NLPLRC---I0KFPKKKCFPFDLPAHQKLAQJELTPDDELEPE---FVQVTEFC 268
 Db 230 IVPKISSLWQTYEGRARDTATEYMSLLESETFPEQVTLHRPCNGD 288

Qy 269 SYIFSHSMTKLPGIMWNGSRKLNLYVNAISSGD-----306
 Db 289 -----ESSGNGVEVKQKXKRDLSFFPAKALEDHKRVANVEAYSRCNCNAEDMGKKL 339

Qy 307 --LPCINENAVLAQRENNSAAVQKAYAHDOQM---OKY-QLPMETLOELDLHRTS 358
 Db 340 WALPCSDANIG---DNIKALD7AVAYEASINGPMKQWQKUSSFLRESVQDL-VHRCG 394

Qy 359 -----ERAEIEVMKNSFKDVD-----QSFQKELETLDAKONDICKRN 397

Db	395 NQMDLMSENSKLKLUQQSLESTMNLKKOLEGREMKKEYQKRYSAID---DICK--	448	Db	2556 QLREEQORQQQME 2569		
Qy	398 LEASSDFCSALSKLUQQSLESTMNLKKOLEGREMKKEYQKRYSAID---DICK--	457	Qy	398 LEASSDFCSALSKLUQQSLESTMNLKKOLEGREMKKEYQKRYSAID---DICK--	457	
Db	449 --LSDOFKNRINDL---ESKCKS1HDE---HSNLMEVGSTR-----LEASE 487		Db	449 --LSDOFKNRINDL---ESKCKS1HDE---HSNLMEVGSTR-----LEASE 487		
Qy	458 VLQKY--LKSKEVSVSHAILQDQALTEKCKKEAQYKAE---AEKAEARLAIAQDN 511		Qy	458 VLQKY--LKSKEVSVSHAILQDQALTEKCKKEAQYKAE---AEKAEARLAIAQDN 511		
Db	48 WKRKYEGTLDENGVSNTRGVDASITRCSNKLIDWIKYENTVSEQAKATEKIAAMEEKL 547		Db	48 WKRKYEGTLDENGVSNTRGVDASITRCSNKLIDWIKYENTVSEQAKATEKIAAMEEKL 547		
Qy	512 EQ-----M0QERBLKHOEQVORMEIAKONWLAEQKHOEQONQFINCFS 557		Qy	512 EQ-----M0QERBLKHOEQVORMEIAKONWLAEQKHOEQONQFINCFS 557		
Db	548 KQASITEDGLRAEFSRVLDEREKITEKAALTLQESTRAELKSAALKV-DECSE 606		Db	548 KQASITEDGLRAEFSRVLDEREKITEKAALTLQESTRAELKSAALKV-DECSE 606		
Qy	558 PUPVTNVRVCCSKEGEAARS 577		Qy	558 PUPVTNVRVCCSKEGEAARS 577		
Db	607 AKDVRLOMSLNLNEKEYESVKS 626		Db	607 AKDVRLOMSLNLNEKEYESVKS 626		
RESULT 9						
Db	G02520		Query Match 5.6%;	Score 171.5;	DB 2;	
	plectin - human		Best Local Similarity 18.7%;	Pred. No. 0.48;		
	C;Species: Homo sapiens (man)		Matches 81;	Conservative 79;	Mismatches 145; Indels 129; Gaps 12;	
	C;Accession: G02520					
	A;Accession: G02520					
	R;McLean, W.H.J.; Smith, F.J.D.					
	Submitted to the EMBL Data Library, March 1996					
	A;Reference number: H01385					
	A;Accession: G02520					
	A;Status: preliminary; translated from GB/EMBL/DDJB					
	A;Molecule type: mRNA					
	A;Residues: 1-1574 <MCL>					
	C;Cross-references: EMBL:U53204; PIDN:91477645; PIDN:91477646					
	A;Gene: PLEC1					
	C;Superfamily: plectin; alpha-actinin actin-binding domain homology <ACT>					
	F;68-283/Domain: alpha-actinin actin-binding domain homology					
RESULT 10						
Db	A59404		Query Match 5.6%;	Score 171.5;	DB 2;	
	plectin [Imported] - human		Best Local Similarity 18.7%;	Pred. No. 0.48;		
	C;Species: Homo sapiens (man)		Matches 81;	Conservative 79;	Mismatches 145; Indels 129; Gaps 12;	
	C;Accession: C59404					
	R;Liu, C.G.; Maerck, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.					
	Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996					
	A;Title: Human Plectin: organization of the gene, sequence analysis, and chromosome loca					
	A;Reference number: C59404; MUID:36210632; PMID:3633055					
	A;Accession: C59404					
	A;Status: preliminary					
	A;Molecule type: DNA					
	A;Cross-references: UNIPROT:Q15149; GB:CAA91196; PIDN:CAA91196.1					
	C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S					
RESULT 11						
Db	2301 DAEMEKKKKPAEQTLRQAEQETLTLRQ-----LEETDHQKNL---2342		Query Match 5.6%;	Score 171.5;	DB 2;	
	250 TLPPDDE-----PEPVQQVTEFCSYIFSHSMTTLPGGIMVNGSRLKNVLTVNAIS 303		Best Local Similarity 18.7%;	Pred. No. 0.48;		
	Db	2343 ---DEELQLRKAATEAARORSQVEEELFSYRVQ-----MEELSKLARIEA-----2386		Matches 81;	Conservative 79;	Mismatches 145; Indels 129; Gaps 12;
	Qy	190 DGQLVTPDEYLENSLRPKQGSQDQYQNFNPLRLC1QKFPPKKCF1FDLPAHOKKLAQLE 249				
	Db	2304 SGDLPC1ENAVLALLQRENSAAVQKAIAYHDQMMG9QVQLPMEIQETLTLRQE-----359				
	Qy	2387 ---ENALILRDKDNTQFLQEEAEAKMVKQVAAEALSVAQAEARLQLAEDLA 2439				
	Db	360 --REALEVFMKNSFDDVQDOSFQKELETLLAKONDICKRNLEASSDYSYCSALLKDFGPLE 417				
	Db	2440 QQRALAEKMKLREKOMQDQVQETRKLRAE-----BLLQQQRELAQDQARRIQQED-----K 2487				
	Qy	418 EAVKQG1SKPGGHNLFQ-----KTEELKAKYKREPRKGQIAEVQLKSK 466				
	Db	2488 EQMAQQLAETQGFTQRTLEAERQRQLEMSAAERKLRLVRAEMSRAQARAEEDAQRFRKQA 2547				
	Qy	467 ESVSHAILQTD-----QALTEPEKKRKAQVRAEAK 498				
	Db	2548 EIGEKLHRTELATEQKVTLYQTLERIQRQOSDHDRLERLRAIAEERKEKLOQZAKLQ 2607				
	Qy	499 AEAQRLAAIQQRQEMQMRERLHQ-----EVYROMETAKQN 535				
	Db	2608 LRSEENQTVQO-----EQVRLQETQALQOSFLSEKDSLLQRERPEKQAKLQFQDVEAKQ 2665				
	Qy	536 WLAEQKMQBQMQ 549				
	Db	2666 QLREEQORQQQME 2679				
RESULT 12						
Db	2230 QQRALAEKMKLREKOMQDQVQETRKLRAE-----BLLQQQRELAQDQARRIQQED-----K 2377		Query Match 5.6%;	Score 171.5;	DB 2;	
	2277 ---ENALILRDKDNTQFLQEEAEAKMVKQVAAEALSVAQAEARLQLAEDLA 2329		Best Local Similarity 18.7%;	Pred. No. 0.46;		
	Db	360 --REALEVFMKNSFDDVQDOSFQKELETLLAKONDICKRNLEASSDYSYCSALLKDFGPLE 417				
	Db	2330 QQRALAEKMKLREKOMQDQVQETRKLRAE-----BLLQQQRELAQDQARRIQQED-----K 2377				
	Qy	418 EAVKQG1SKPGGHNLFQ-----KTEELKAKYKREPRKGQIAEVQLKSK 466				
	Db	2378 EQMAQQLAETQGFTQRTLEAERQRQLEMSAAERKLRLVRAEMSRAQARAEEDAQRFRKQA 2437				
	Qy	467 ESVSHAILQTD-----QALTEPEKKRKAQVRAEAK 498				
	Db	2438 EIGEKLHRTELATEQKVTLYQTLERIQRQOSDHDRLERLRAIAEERKEKLOQZAKLQ 2497				
	Qy	499 AEAQRLAAIQQRQEMQMRERLHQ-----EVYROMETAKQN 535				
	Db	2498 LKSEENQTVQO-----EQVRLQETQALQOSFLSEKDSLLQRERPEKQAKLQFQDVEAKQ 2555				
	Qy	536 WLAEQKMQBQMQ 549				

A;Gene: CESP: F48F5.1	A;Molecule type: mRNA
A;Map position: 5	A;Residues: 1-1690
A;Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3	A;Cross-references: EMBL:AF041382; NID:92773362; PIDN:AAB96783.1
Query Match 5.3%; Score 160.5; DB 2; Length 1291; Best Local Similarity 18.7%; Pred. No. 0.38; Mismatches 100; Indels 224; Gaps 31; Matches 143; Conservative 100; Mismatches 224; Indels 299; Gaps 31;	A;Experimental source: strain Oregon R
Qy 14 IENFNEOLK- Score 160.5; DB 2; Length 1291; Db 287 LSRYNEKLKSTFPADNAROYQSFNSQFKESSFSVPTDAVASGVIAEYKRC- -CNHLGG 341.	C;Genetics:
Qy 61 -----KNGKGSVASTVQSPHTKGIMWCYPHNWNHTLVLL---DTGSLGIVDEKADNK 110	A;Cross-references: FlyBase:FBgn0020503
Db 342 PQTDDERRPGHEFMVKGS-----VGDSLIAHMSQTALDQLEK- -382	C;Keywords: cytoskeleton
Qy 111 NDQIFALAL-----LISSTFVNTYNTKIDOGA- -IDLNENYNTELTDLLKARNSPDL 160	Query Match 5.3%; Score 160.5; DB 2; Length 1690; Best Local Similarity 20.8%; Pred. No. 0.54; Mismatches 114; Conservative 90; Mi smatches 185; Index 159; Gaps 26
Db 383 -DVADEVKVLSTFTDINNQIISSEGIVKVDIKSGKLAKIQENVKNSIEKINGIKLKL 441	Matches 104 VEKADNKNDIQIFALALLISSTFVNTYNTKIDOGAIDL---LANTTEFLDLKARNSPDL 160
Qy 161 DRVEDPADSASFFPDVLWVTLRDFCLGLEIDDGOLYTPDEYLNLSRPKQGSDQRYVNENLP 220	Db 385 VERDIDREDAQNOQL-----QKNIELKARIVELAEGNRKKTTEELQC---SI 433
Db 442 ESTLPLNNSFIQDVMFK-----EVITAETSVG-----471	Qy 161 DRVEDPADSASFFPDVLWVTLRDFCLGLEIDDGOLYTPDEYLNLSRPKQGSDQRYVNENLP 220
Qy 221 RLCIOKFPKKKKCF FDLPAPHQKKAQELTLPDDELEPPVQOTTEFCXYIFSHSM--TK 278	Db 434 DEAQ-----FC-GDELNAQSQVYKEKIH-----LESKITKLVSA 467
Db 472 --CLQK-LRKSLLVTOQIATQIOLKRL---DDKL-LIESVQQTAKVSQ-FSETLASTK 522	Qy 221 RLCIOKFPKKKKCF FDLPAPHQKKAQELTLPDDELEPPVQOTTEFCXYIFSHSM--TK 278
Qy 279 TLPGGGMVNGSRLKRNLYTVNAISSGDLPCIVNLAQNSAAYVAAIAH-----332	Db 468 TPSLQSLIPPP-----DLPSDDGAQEEIAQLQEMTIOQKEVRSRIABOLEEBORLREN 521
Db 523 KIPDAMKRN-----VKNVTLENKRSSELSLNQSDAISHSASAR 560	Qy 268 CSYIISHSMTKTLPGIIMYNGSRSLKRNLYTVNAISSGDLPC-1EN- -AVLALAQRENSA 324
Qy 333 -----YDQOMGQ-----KYLQPMLE- -TQELFLDLHRTS- -EREATIEVFNK 368	Db 522 VKYL- -NEQATLQSELVSKDEALEKFSL-----EGC1ENRRELALLKEENK 569
Db 561 SVFGLVYKLESSIGQLNDTIVSSETDKIKIKAEPKMKLQLWGNHETGVNLSQAVVQAK 620	Qy 325 AVQKIAHYDQMGKQVQLEMETLQBLDDLHRTS-----EPEAI-----EPMKRN- 369
Qy 369 NSFKDQDQS-----POKELETTLLDQK-----390	Db 570 QAQEQQAEFTKLAKSVEVTRISSELSQNLKATSSLSERENVKSDCECELQTERMRDE 629
Db 6221 AFVAKIDVSKLKLTKLNNYSAALKTLEMPYTMMEALEKSEVLEILIRRAISATRRERRRAAG 680	Qy 370 SFKDVTDQSFQKELETTLLDQKQNDICKRNLLEASSDYSCLALKDIFCPPLERAVKQGYSKPG 429
Qy 391 -----NDICKRNLEASSDYC-----SALLKDIFGPLEAVKGQIVS 426	Db 630 QIRELNQQLD-EVITVQLNQVQKAD-----SSALDDML---RIQKEGTBEK- -669
Db 681 SNAHLVAAKVLQDQFLQSSNTIAHFKNAPLAFQSFSSKFLAKF- -AQQQKISA 735	Qy 430 GHNLFIQKTEELKAKYKREPRKGQIAEEVQKYLK-----464
Qy 427 KPGG-----HNLFI 435	Db 670 --STILEKTEKEVYQIKEQAKTILQDKEQLEKQI-----AORLAAICQRNEQ 513
Db 736 SQNGGGGGSESEFPTVIVVSV1VGALLLALLAFLAFLFLYGFHQKQAKIDRNKEI 795	Qy 465 SKESTVSHALQTDLQALTETEKKKKPAQVKAEEKAE-----728 EKESSEQQLALKQNLQEDFQKKQSESEVHQLQELQAKNTQDLEQVREXTENAINQIQL 727
Qy 436 QKTEELKAKYKREPRKGQIAEEVQKYLKSESHI-----LOTDQL 480	Db 788 KTLGHEKL---QAALELKEKETTILIKEKEQELQQLQSKSAESESAALKVQVQLEQLOQQ 844
Db 796 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	Qy 565 VCSSSKEG 572
Qy 481 TETEK-----KREAQVKAQVKAEEKAQRLAAIQRQNEQMMOERERLHQEVQRM 529	Db 845 AAASSEEG 852
Db 856 SEARKIAEKKKDEQNEKEKAQKLRADEQKSEARKYAE-KKQDEQNEKEKAQKLRADEQ 914	RESULT 13
Qy 530 EIAKONWLAECQKMEQOQMOVFINCF--ISPLP- VTMVRCCSGKEG 572	A39638 Plectin - rat
Db 915 EKSEARKIAEKKKDEQNEKEKAQKLRADEQKSEARKYAE-KKQDEQNEKEKAQKLRADEQ 960	Species: Rattus norvegicus (Norway rat)
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Primary
Qy 481 TETEK-----KREAQVKAQVKAEEKAQRLAAIQRQNEQMMOERERLHQEVQRM 529	A;Species: mRNA
Db 856 SEARKIAEKKKDEQNEKEKAQKLRADEQKSEARKYAE-KKQDEQNEKEKAQKLRADEQ 914	A;Residues: 1-4687 <WIC>
Qy 530 EIAKONWLAECQKMEQOQMOVFINCF--ISPLP- VTMVRCCSGKEG 572	A;Cross-references: UNIPROT:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Db 915 EKSEARKIAEKKKDEQNEKEKAQKLRADEQKSEARKYAE-KKQDEQNEKEKAQKLRADEQ 960	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
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Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Species: Drosophila melanogaster
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Reference number: A39638; MUID:91268156; PMID:2050743
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Accession: A39638
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
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Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Cross-references: UniProt:P30427; EMBL:X59601; NID:9129885; PIDN:CAA42169.1
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	C;Accession: A39638; Alpha-actinin actin-binding domain homology; ribosomal R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.
Db 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	J. Cell Biol. 114, 83-99, 1991
Qy 916 DDEIEEARQEEENQIAQKNALEAKIKKEKSNNRKVWDEQNEQKEDLQAKLRADEK 855	A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide o

Query Match	5.3% Score 160.5; DB 1; Length 4687;	Qy	182 DPCUGLEIDGOLYTPDEVYELNSL-----RPGQSDQFVNFLPRCQKFFP 222	
Best Local Similarity	18.3% Pred. No. 1, 9; Mismatches 143; Indels 135; Gaps 13;	Db	194 DH-TG-----VPLANLRLNTLQDNLTHIWSSSKPGALENSKIEDY-----234	
Matches 80; Conservation 79; Mismatches 143; Indels 135; Gaps 13;				
190 DGQVTPDEYLENSLRPKGSDORVQNFNLPRLCIQLKPKKKCFIFDLPAHOKKLAQE 249		Qy	195 KKRCPFDLPAHOKKLAQEFLDPEFVQVTERCSYIFPSHSMTKLPGGIMVNGS 283	
2304 DAENBKHKKPAAEPTLQRQKQVEQFLTLRQ-----LBDTHQKSIL---2345		Db	230 KKRCPFDLPAHOKKLAQEFLDPEFVQVTERCSYIFPSHSMTKLPGGIMVNGS 283	
250 TLPDDELE-----PEFVQVTECSYIFPSHSMTKLPGGIMVNGSRLKNLVITYNIS 303		Qy	234 FDEFAALPHKLQ---FD-----KFISEVQNL-----GSRPFIAGH 266	
2346 ---DEELQRLKAETEAAQRQSYEEELFS-----VRQMEELGK-L-KARIEA--2389		Db	290 RLKNLVITYNVAISGDLPCIENAVLAQRENSAAVQKAIAHYDQOMCQKQVLPMTLQ 344	
304 SGDLPCIENAVLAQRENSAAVQKAIAHYDQOMGOKVQLPMETLQ-----2359		Qy	267 RNKD-----SDATDQELTGGFFP-----284	
2390 -----ENRALLRLDKNTQRFLEEEAKMKQVAEEAARLISVAQEARLRLQAEELA 2442		Db	350 ELLDLHRTSEREAIEVMKN-----SFKVDVQDOSFQKELETLDAKONDICKRNLEAASSD 403	
360 --REALEYFVMKNSPKDVOQSFKDOSFQKELETLDAKONDICK--RNLEASSDYCALSALKCIG 414		Qy	287 --EYHRRIPADGKQDSSIVAYEIGWINDQIVSNKDLQDLPQE---LIAQFRCDIEARVQIAFD 344	
2443 QQRALLAEKMKLKERQVAQEPATRILKAEEALLQOKEELAQEQRRLQAD-----2489		Db	404 YCSMALLKQJFGPLEEAVGQIYSPGP---GRNLFLQTEELKAKYR--EPKGQIAE 455	
4115 PLEBAVKQGCIYSKPGGHNLFQ-----KTEBKAKYVREPRKGQIAEEVLOXYL 463		Qy	341 RAAAPLLEBQQAESTRAGPKAVPLNLQGIGAEEAREKCVRNPFQASRYRHKGVYTKRAELE 400	
2490 --KEQMAQOLVETOGFQRTLEAERQRQLEMSAEEAERLKLRAEMSRAQARAEEDAQRFR 2547		Qy	457 EVLQKYKKS-----KESVSHAILOQTQ-----LTETEKKKKEAQ 491	
464 KSKESVSHAILOQT-----QALTETEKKKKEAQYKAE 495		Db	401 DKDNRLLKALYQHLLTAHKGATYFAETEVKRTKTLI 466	
2548 KQABEIGEKLHRTELATEQKVTLVQTLTQDQABRLREAELEREKEKLKOZAK 2607		Qy	492 VKAEEKAQRLAIAIQRQNEQMMEQRE-----RHOEVQRMEMIAKQNLIAQKRNQ 545	
496 AEEKAQRLAIAIQRQNEQMMEQERLHQ-----EYQVROMEIA 532		Db	461 FKEKEAOSLAIQPGWASNPKPQVLFKEKELDEVSARLRLCEEMRRAIRVWRSR-----515	
2608 LLQQLKSEMENQTVQO-----EQIQLQETQALQSFSLSEKDSLQLRERFIEQEEAKLQFQDEVA 2665		Qy	546 QDQVFVINCFSIPFVITMRVCSSGEGAAARSQCG---SQQGWSQRKV 590	
533 KQWLAQEQKMQEQQMQ 549		Db	516 -----LGDAIGLEFNKLGSRGSSGAPESGEKPKATEKD1W-DRWV 554	
2656 KAQLOQEEEQORQQQME 2682			RESULT 15	
			H30279	
			microtubule binding protein, probable [imported]	
			C:Species: Sulfolobus solfataricus	
			C:Date: 24-May-2001 #text_change 09-Jul-2004	
			C:Accession: H90279	
			R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.; Jong, I.; Jeffries, A.; Kozena, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Verhaert, R.A.; Ragan, M.A.; Senes, C.W.; Van der Oost, J.	
			Submitted to GenBank; April 2001.	
			A:Description: Sulfolobus solfataricus complete genome.	
			A:Reference number: A99139	
			A:Accession: H90279	
			A:Status: preliminary	
			A: Molecule type: DNA	
			A:Residues: 1-464 <KUR>	
			A:Cross-references: UNIPROT:Q9UXN4; GB:AE006641; PIDN:AAK41495; PIDN:AAK414951	
			C:Genetics:	
			A:Gene: SSO1256	
			Query Match 5.2% Score 158; DB 2; Length 464;	
			Best Local Similarity 23.0%; Pred. No. 0.14; Mismatches 136; Indels 68; Gaps 17	
			Matches 85; Conservative 81; Mismatches 136; Indels 68; Gaps 17	
			251 LPDDEL-----EPFEPVQVTFCSYIFSH---SMTKLPGGIMVNGSPKLNVLITYVNAI 3024	
			Qy	2 LKDDILKLLKDAEPRKQVEETIGLSPINVTLADKLQDILKGLASMDKLKSSYDOLVDAQ 61
			Db	303 SSSD-LPCIENAV-----LALAQRENSAAVQKAIAHYDQOMGQVLPMTLQELLDLHRTS 358
			Qy	62 RRAEERIAKLENRAVEQVLVEAQRTDERITKL---ESTKLE---QAVQELLEAQKHH 113
			Db	359 EREAEIYFMKNSPKDVOQSFKDOSFQKELETLDAKONDICKRNLEAASSDYSCLSKDIFGPQLES 418
			Qy	114 DERITKLE---ESTKLE-----QKRDHERITKLEESTKLE-----KLEQ 157
			Db	419 AVKQGYSKPGGHNLFLQKTYREPKQKIAEEVQKYLKSKEVSQHAILOQTQ 478
			145 LIINWIEHOVGLYQGANGLLKTIVFVNMLQFQDQDFKPSKDKONIOT-----SLLF 216	
			145 LIINWIEHOVGLYQGANGLLKTIVFVNMLQFQDQDFKPSKDKONIOT-----SLLF 216	

Qy	479	ALPETEKKE-----AQYKAEEKAQRLAAIQORNEOMQERBLHQ	523
Db	217	ELIAQKHDERITKLEESTKKLEAQVQELIAQKHDERITKLEESIQKLVDQRAE	275
Qy	524	EQVROQMEIAKQNLIAEQQMKMEOQMVOQFINCFISPL-PVTMRVCSQ--GKEG--EAARS	577
Db	276	ERIAQLENVEQ-LVEAQKRTDER-----ITLKEEVTMKLVESQLMQNEIRSLRKA	326
Qy	578	CGSQCGVNSQ	587
Db	327	LGNGKRNCR	336

Search completed: May 20, 2005, 13:28:53
Job time: 46 secs

Db	RESULT 5	GBP1_HUMAN	STANDARD	PRT;	592 AA.
Qy	470	SHAIQDQALTEKKCKKEAQVKAEEAKAQLAAQRAQNEQQMERLHQEQVROM	529		P32-55;
AC		DT 01-OCT-1993 (Rel. 27, Created)			
DT		DT 01-OCT-1993 (Rel. 27, last sequence update)			
RA		DT 25-OCT-2004 (Rel. 45, last annotation update)			
RA		DE Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)			
RA		DE (Guanine nucleotide-binding protein 1) (HUGBP-1).			
RA		DE Name=GBP1;			
RA		OS Homo sapiens (Human).			
RA		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
RA		RA Mammalia; Buthynia; Primates; Catarrhini; Hominidae; Homo.			
RA		NCBI_TaxID=9606;			
RN		RP SEQUENCE FROM N.A.			
RX		RA MEDLINE=91342675; PubMed=1715024;			
RA		RA "Interferon-induced guanylate-binding proteins lack an N(T)XRD			
RA		RA consensus motif and bind GMP in addition to GDP and GTP.";			
RA		RA Mol. Cell. Biol. 11:4717-4725(1991).			
RN		RP SEQUENCE FROM N.A.			
RA		RA Kalanine N., Chen X., Rolfs A., Halleck A., Eisenstein S.,			
RA		RA Koundinya M., Raphael J., Moreira D., LaBarre J., Lin Y.,			
RA		RA Phelan M., Farmer A.,			
RA		RA "Cloning of human full-length CDSS in BD Creator(TM) system donor			
RA		RA vector.";			
RA		RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
RN		RP SEQUENCE FROM N.A.			
RA		RA TISSUE=Uterus;			
RX		RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA		RA Stansberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA		RA Klaunser R.D., Collins P.S., Wagner L., Shanmen C.M., Schuler G.D.,			
RA		RA Altschul S.F., Zeeberg B., Bueton K.H., Schaefer C.F., Bhat N.K.,			
RA		RA Hopkins R.F., Jorden H., Moore T., Rubin G.M., Hong L.,			
RA		RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,			
RA		RA Stapleton M., Soares M.B., Bonaldo M.F., Carlson P., Prange C.,			
RA		RA Brownstein M., Usdin T.B., Toshiyuki S., Mullaly S.J.,			
RA		RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D.,			
RA		RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA		RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA		RA Villalobos D.K., Mizny D.M., Sodergren B.J., Lu X., Gibbs R.A.,			
RA		RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,			
RA		RA Whiting M., Madan B., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA		RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,			
RA		RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA		RA Butterfield Y.S.N., Krzywinski M.I., Skalnik U., Smilus D.E.,			
RA		RA Schnerch A., Schein J.E., Jones S.J.M., Marrs M.A.;			
RA		RA "Generation and initial analysis of more than 15,000 full-length human			
RA		RA and mouse cDNA sequences";			
RA		RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN		RP ISOPRENOID.			
RX		RA MEDLINE=96427476; PubMed=8830800;			
RA		RA Nantais D.E., Schwenmke M., Stichney J.T., Vestal D.J., Buss J.E.;			
RA		RA "Prenylation of an interferon-gamma induced GTP-binding protein: the			
RT		RT human guanylate binding protein, huGBP1.;"			
RT		RT J. Leukoc. Biol. 60:423-431(1996).			
RL		RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			

PT	STRAND	286	287	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone 5330409J06 product:weakly similar to GUNYLATE BINDING PROTEIN 5.
PT	STRAND	289	289	
PT	HELIX	290	306	
PT	TURN	307	307	
PT	STRAND	311	311	
PT	HELIX	312	342	BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]
PT	HELIX	350	371	
PT	HELIX	376	378	
PT	HELIX	379	423	
PT	TURN	424	427	SEQUENCE FROM N.A.
PT	TURN	430	431	STRAIN=C57BL/6J; TISSUE=Pituitary gland; PMID=9279233; DOI=10.1016/S0076-6879(93)03004-9;
PT	HELIX	432	449	RA
PT	TURN	455	456	RA
PT	HELIX	457	467	RT
PT	TURN	468	468	RL
PT	HELIX	469	478	RP
PT	HELIX	484	563	SEQUENCE FROM N.A.
PT	TURN	564	564	STRAIN=C57BL/6J; TISSUE=Pituitary gland; PMID=21085660; DOI=10.1038/35055500;
PT	HELIX	566	582	RA
SQ	SEQUENCE	592	AA;	RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; RN
Qy	MALEIHMSPGMLIENNEQLKVNQBALEILSAILTQPVWVVAIVGLYRTGKSYLANKLAG	60	60	RP
Db	1 MASEIIRNTGPMCLIENTNGRMLANPEALKSILSAITQPVWVVAIVGLYRTGKSYLANKLAG	60	60	SEQUENCE FROM N.A.
Qy	61 KNGKGFISVATSYQSHTKGWINGVCPHPNPNTLVLIDTEGLDVEKAIDKNDIQIFALL	120	120	SEQUENCE FROM N.A.
Db	61 KKKGFISLGSVTSQSHTKGWIWNGVCPHPNPNTLVLIDTEGLDVEKAIDKNDIQIFALL	120	120	SEQUENCE FROM N.A.
Qy	121 LLSSTPVTYNTKIDOGAIDLHNTTELDTLKHARNSPD--LDRYEDPAUSASFPDLWV	178	178	SEQUENCE FROM N.A.
Db	121 LLSSTPVTNSGTINQAMDQIVYVTEHLTHIRSKSPDENENEVEDSADEVSFFPDPFWV	180	180	SEQUENCE FROM N.A.
Qy	179 TLRDFCLGLEDQGLVTPDEYLENSLRPKQGSSDORYVNENLPRCLQKFRPKKKCFIFDL	238	238	SEQUENCE FROM N.A.
Db	181 TLRDFSLDLEADQGPUPDPEYLTSLKLKKTQSDDETFLNPLRCLTRKFPKKCFVDFR	240	240	SEQUENCE FROM N.A.
Qy	239 PAHQKLLAQETLTPDDELEPEPQVQTYTFCSYIIFSHSMKTLPLGGIMVNSRLKNUVLT	298	298	SEQUENCE FROM N.A.
Db	241 PVHRRKLAQELKQDPELDPFVQVADFCSYIFNSNSKTKLSSGGIQVNGPRLESVLT	300	300	SEQUENCE FROM N.A.
Qy	299 VNAISSCDLPCLENAVLAQRENSAQAOKATAHYDQMGKQVLPMTMQLBLHRS	358	358	SEQUENCE FROM N.A.
Db	301 VNAISSCDLPCLENAVLAQIENSAQAOKATAHYDQMGKQVLPTESQBLBLHRS	360	360	SEQUENCE FROM N.A.
Qy	359 EREAIEVMKNSFKDQVDSQFEKOLETILDAKONDICKRNLFASSDYCSAIIKDFGPIE	418	418	SEQUENCE FROM N.A.
Db	361 EREAEVFIRSSFKDQVDFLHQLKEALAQLERCRDDFCQKONQEASSDRCSGQIQLVSPBLE	420	420	SEQUENCE FROM N.A.
Qy	419 AVKQGQYSKPGCHNLFTQKTEKBLAKYREPRKGIAEVILQYKLSKESVSHATLQDQ	478	478	SEQUENCE FROM N.A.
Db	421 EVKAGIYSKPGCHNLFTQKTEKBLAKYREPRKGIAEVILQYKLSKESMSTDALQTDQ	480	480	SEQUENCE FROM N.A.
Qy	479 ALTETEKKKAQKAEEKAQAAIAIQQNENQMQERERLHQEVQRO---MEIAKQ	534	534	SEQUENCE FROM N.A.
Db	481 TLTKEKEIIEVERVKAESAQSASKMLQEMQRNEQMMEQKERSYOSHOLTERMENDRV	540	540	SEQUENCE FROM N.A.
Qy	535 NWLAEQQ-----KMQEQQ	547	547	SEQUENCE FROM N.A.
Db	541 QLLKEQERTALALKLQEQE	558	558	SEQUENCE FROM N.A.
RESULT 6	Q8BNM7	PRELIMINARY;	PRT;	724 AA.
AC	Q8BNM7;			
DT	01-MAR-2003	(TrEMBLref. 23; Created)		
DT	01-MAR-2003	(TrEMBLref. 23; Last sequence update)		
DT	01-MAR-2004	(TrEMBLref. 26; Last annotation update)		

DR	GO:0006955; P:immune response; IEA.	RA	Nguyen T.T., Hu Y., Widney D.P., Mar R.C., Smith J.B.; "Murine GBP 5, a new member of the murine guanylate-binding protein family, is coordinately regulated with other GBPs in vivo and in vitro.,"
DR	InterPro: IP0003191; GBP.	RT	"Murine GBP 5, a new member of the murine guanylate-binding protein family, is coordinately regulated with other GBPs in vivo and in vitro.,"
DR	Pfam: PF02263; GBP; 1.	RT	"Murine GBP 5, a new member of the murine guanylate-binding protein family, is coordinately regulated with other GBPs in vivo and in vitro.,"
DR	Pfam: PF02841; GBP; 1.	RT	"Murine GBP 5, a new member of the murine guanylate-binding protein family, is coordinately regulated with other GBPs in vivo and in vitro.,"
SQ	SEQUENCE 724 AA; 80410 MW; 799C517B51DBF47C CRC64;	RL	J. Interferon Cytokine Res. 22:899-909 (2002).
Query Match	Score 1933; DB 2; Length 724;	RN	RN [2].
Best Local Similarity	63.5%; Pred. No. 8 Be-90;	RN	RN [2].
Matches 392; Conservative 70; Mismatches 126; Indels 16; Gaps 5;	RN	RN [2].	
Qy	1 MALBIIHSDPMCLLIEFNQELKYNQNEALEBILSATTOPVVVAVLGlyRTGKSYLMNKLAG 60	RN	RN [3].
Db	1 MAPEHIMPPPLCLIGSTSEGHVLTNQEAKILSATTOPVVVAVLGlyRTGKSYLMNKLAG 60	RN	RN [3].
Qy	61 KNKGFPSVASTQSHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120	RA	SEQUENCE FROM N.A.
Db	61 KEKGFPSVASTQSHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120	RA	SEQUENCE FROM N.A.
Qy	121 LLSSTFVNTVNKIDQAGADLILANVTELDLILKARNSDLDYR-EDPADSASFFPDIVW 178	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	121 LLSSTFVNTVNKIDQAGADLILANVTELDLILKARNSDLDYR-EDPADSASFFPDIVW 178	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Qy	179 TLRDFCLGLEIDGOLVTPDEYLNSLRPKQGSDORVNENLPLCIOKFFPKKKCF1FDL 238	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	180 TLRDFCLGLEIDGOLVTPDEYLNSLRPKQGSDORVNENLPLCIOKFFPKKKCF1FDL 238	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Qy	239 PAHOKKLIAOLETLFDDDELPEPEFYQVTTPEYDLENSLRPKQGSDORVNENLPLCIOKFFPKKKCF1FDL 298	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	240 PALGSKLQSPLTSNEEINSDFYQDLSSEFCSHFTQSTKTKLPGGIONGPRLESVLYT 299	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Qy	299 VNALSSGDPICENAVLLAQRENSAAVQAKIAHYDQNGQKVLQPMETLQELLDIHTS 358	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	300 VDANSGALPSIENVTARRENSAVQAKIAHYDQMLSEKVPPTLQELLDIHTS 359	RA	STRAIN-NMRI; TISSUE=Breast tumor; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Qy	359 EREATEFNMKNPSKFDVDSOFSQKELETLIDAKNDICKNLEASSDYSALLKDFGPEE 418	CC	-1-SIMILARITY: Belongs to the GBP Family.
Db	360 EREATEFNMKNPSKFDVDSOFSQKELETLIDAKNDICKNLEASSDYSALLKDFGPEE 419	CC	-1-SIMILARITY: Belongs to the GBP Family.
Qy	419 AVKGQIYSSKGHHNLFIQTEELKAKYREPRKGQIAKEVLYKLSKESVSHALQDQ 478	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	420 EVAQEYHFKPGGHKLFLQRMEEQKANRQPGKGTQAEFLQTYLNAKETVSTLQDQ 479	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	479 ALTETEKKKEAQYKAAKAAEAKAORLAIAQRLQNEQMWERERLHQEQTRMATAKONTLA 538	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	480 VLTTEKELIQSKAQEQRRAELEARLQEAIRIQLQEQKEMERHQEQRQIALEKARYQ 539	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	539 EQQRMQEQQMQ---VFINCFTISPL-----PVTMRCVSSGKGEARSCSGQQGWSQ 587	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	540 EQQWILKQRAQGRCPVWCLLIAEDBGPQDLSQKLCFGQEG--GRLSGRDEGAASE 597	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	588 KVVW 591	DR	EMBL; AF422443; AAC31451.1; -
Db	588 ALWI 601	DR	EMBL; AY128412; AAC4632.1; -
RESULT 7		DR	EMBL; BC58555; AAH58555.1; -
ID	GBP5_MOUSE STANDARD; PRT; 590 AA.	FT	HSSP; P32455; 1DG3.
AC	Q8CB4; Q8CFA4.	FT	MGI; MGI:2423943; Gbp5.
DT	29-MAR-2004 (Rel. 43, Created)	FT	InterPro; IPR03191; GBP.
DT	29-MAR-2004 (Rel. 43, Last sequence update)	FT	PFAM; PF02263; GBP; 1.
DT	05-JUL-2004 (Rel. 44, Last annotation update)	FT	PFAM; PF02841; GBP; 1.
DE	Interferon-induced Guanylate-binding protein 5 (GTP-binding protein 5) (MugBP-5).	FT	GRIP; GRIP; 1.
DE	(Guanine nucleotide-binding protein 5) (MugBP-5).	FT	GRIP; GRIP; 1.
GN	Name=GBP5;	FT	GRIP; GRIP; 1.
OS	Mus musculus (Mouse).	FT	GRIP; GRIP; 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	FT	GRIP; GRIP; 1.
OX	[1]	FT	GRIP; GRIP; 1.
RN	SEQUENCE FROM N.A.	FT	GRIP; GRIP; 1.
RN	STRAIN=Svis8 Webster;	FT	GRIP; GRIP; 1.
RN	STRAIN=Swiss Webster;	FT	GRIP; GRIP; 1.
RN	MEDLINE=22284156;	FT	GRIP; GRIP; 1.
RX		FT	GRIP; GRIP; 1.
Qy	1 MALEIHMSDPMCLLINFNEBQLKYNQEALEBILSATTOPVVVAVLGlyRTGKSYLMNKLAG 60	Qy	1 MALEIHMSDPMCLLINFNEBQLKYNQEALEBILSATTOPVVVAVLGlyRTGKSYLMNKLAG 60
Db	1 MAPFHMPEPLCLIGSTEGHLVNTQALKLISATTOPVVVAVLGlyRTGKSYLMNKLAG 60	Db	1 MAPFHMPEPLCLIGSTEGHLVNTQALKLISATTOPVVVAVLGlyRTGKSYLMNKLAG 60
Qy	61 KNKGFSVASTVQHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120	Qy	61 KNKGFSVASTVQHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120
Db	61 KERGFPSVSTVQHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120	Db	61 KERGFPSVSTVQHTKGIMWCPHNPNTKLYLDPTEGLGVEAKNDQIFAL 120
Qy	121 LLSSTFVNTVNKIDQAGADLILANVTELDLILKARNSDLDYR-EDPADSASFPDLW 178	Qy	121 LLSSTFVNTVNKIDQAGADLILANVTELDLILKARNSDLDYR-EDPADSASFPDLW 178

Db	121	LISSTFVNTKNDQGATDULHNTTELDTLRTNSDSNOTECEGPAD-MSFPFDLV	179	RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Qy	179	TLDFFCGLDQVTPDEYLENSRKPQGSDQRYQNFNLPRLC1QKFPPKKCFTFDL	238	RT	
Db	180	TLDFFLDLQANGHATSDDEYLENSLKLKGQSDERTOTFLPRLC1QKFPPKKCFTFD	239	RL	
Qy	239	PAHQKQLAQLQETLPDDELEPEFVQVQTEFCSYIFSHSMTKULPGGIMVNGSRLKVLVLY	298	RN	
Db	240	PALGSKLSQPLPSNEELNSDDEVQDLSFCSHIFTSKTLPGGIQVNGPRLESVLY	299	RP	SEQUENCE FROM N.A.
Qy	299	VNAISSCDLPCTENAVLAORENSAVQKIAHYDQMGOKVQLPMEIQBLQDILHRTS	358	RC	STRAIN=CS7BL/6J; TISSUE=Lung; MEDLINE=2030913; PMID=11076861; DOI=10.1101/gr.152500;
Db	300	VDAINSGLAPSNTENVTLARRENSAAVQKIAHYDQMLMSKVPQLTETQBLQDILHRTC	359	RX	RA
Qy	359	BREATIVEFVQKSFQDYNQSFQNELETLDAKONDICKRNELASSDCSALLKDTGPLE	418	RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishida T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi M., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.";
Db	360	EREAIEFPRKSFQDGFQFQXELSSLSAKQDEIKRNADASAAICSTLGSIPKPLE	419	RT	Genome Res. 10:1757-1771(2000).
Qy	419	AVKQGITYSKPGCHNLP1QKTEPELAKYREPRKG1QAEVILQKYLKSKEVSYHAI1QTDQ	478	RL	[6]
Db	420	EVAQEPYHKPGCHNLP1QKTEPELAKYREPRKG1QAEVILQTYINAETKTSR1LQTDQ	479	RP	SEQUENCE FROM N.A.
Qy	479	479 ALTTETKKEKAQVKAEEKAQEAEQARLAAQBQNEQMMQERERLHQEQVRQMEIAK-----	533	RC	STRAIN=CS7BL/6J; TISSUE=Lung; Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hizukuri S., Hiyama K., Hayatsu N., Hiramoto K., Hirakawa T., Hirozane T., Hishida H., Hayashi K., Hayashi T., Imotani K., Ishii Y., Itoh M., Kagawa I., Kashiwagi M., Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito C., Saito K., Saito S., Saito Y., Saito Y., Saito Y., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muranatsu M., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.";
Db	480	VLTDEKIQKKEQEREAARLAKQLEAARIQEQKAEWERMHQEQRLQIALEKARVQ	539	RA	Submitted (APR 2002) to the EMBL/GenBank/DBJ/GenBank databases.
Qy	534	-QNWLAEQQRKQNE 545		RA	
Db	540	EQQWILKQRQDQE 552		RA	
RESULT 8					
Q8BU78		PRELIMINARY;	PRT;	561	AA.
ID	Q8BU78;				
AC	Q8BU78;				
DT	01-MAR-2003	(T-EMBL)reel. 23, Created)			
DT	01-MAR-2003	(T-EMBL)reel. 23, Last sequence update)			
DT	01-MAR-2004	(T-EMBL)reel. 26, Last annotation update)			
DE	Mus musculus	0 day neonate lung cDNA library, clone E030025M22 product:weakly similar to GUANYLATE BINDING PROTEIN 5 (Fragment).			
DE					
GN	Name=Gbp5;				
OS	Mus musculus (Mouse);	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;			
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6J; TISSUE=Lung; MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RX	"High efficiency full-length cDNA cloning.";				
RT	Meth. Enzym. 30:19-46(1999).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6J; TISSUE=Lung; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505550;				
RA	RIKEN FANTOM Consortium;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 403:685-690(2001).				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6J; TISSUE=Lung;				
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6J; TISSUE=Lung;				
RA	SEQUENCE FROM N.A.				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
Qy	299	VNAISGGDLPCTENAVLAQORENSAAVQKAIHYDQMGQKVPMTQELLDLHRTS	358	Qy	
Db	300	VDAINSGLAPSNTENVTLARRENSAAVQKAIHYDQMLSEKVPQVQPTETLQELLDLHRTC	359	Db	

359 EREAEIVFMKNSFKDVSOSFQKELETILDAKONDICKNLASSDYCSALLKIDFGLLEE 418
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DR 360 EREAEIEIRKHSFKDEGGFFQKLELSLISAKDDEICKNADISAALCSTLLGSIFKELEQ 419
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DR 419 AVKOGIYSPKGHNLFQITKEELKAKTYREPRKGQIAFEVLOKYLKSKEVSHTAILQDQ 478
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DR 420 EVAQEYHKPGGHKLFLORMEQLKANTYRQQPGKGTQAEVLOTYLNAKETVSRILQDQ 479
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DR 479 ALIETEKECKKEAQYKAEEAKAERLAAIQRONEQMCERELHQEQRMELAKONWLA 538
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DR 480 VLTDEKEIQSKAEEAARLEQLEAFRQLEAIRQEEQRKAEEMERHQEQRLQIALEKARVAQ 539
 Qy :|||: :|||: :|||: :|||: :|||: :|||:
 DR 549 EOKKMQEQQMQ 549
 Qy :|||: :|||:
 DR 540 EQQWILKQRAQ 550

RESULT 9

GBP2_HUMAN STANDARD; PRT; 591 AA.

AC P32456; 086780;
 DT 01-OCT-1993 (Rel. 27, Created)
 DR 01-NOV-1995 (Rel. 32, Last sequence update)
 DR 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-induced Guanylate-binding protein 2 (GTP-binding protein 2)
 DE (Guanine nucleotide-binding protein 2) (RugCBP-2).
 CN Name=GBP2;
 CS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN SEQUENCE FROM N A.
 RP MEDLINE:911312675; PubMed=1715024;
 RA Cheng Y.-S.E., Patterson C.E., Staeheli P.,
 RT "Interferon-induced Guanylate-binding proteins lack an N(T) KRD
 consensus motif and bind GMP in addition to GDP and GTP.";
 RL Mol. Cell. Biol. 11:4717-4725 (1991).
 [12]
 RN REVISIONS.
 RC TISSUE:Reskin;
 RA Schwemmle M;
 RL Submitted (SBBP-1991) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N A.
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
 RA Wiemann S;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Binds GTP, GDP and GMP.
 CC -!- INDUCTION: By interferon gamma during macrophage activation.
 CC -!- SIMILARITY: Belongs to the GBP family.
 CC
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 or send an email to license@isb-sib.ch).

DR EMBL; M5543; AAA67323.1; -.
 DR ALB32451; CDD89925.1; -.
 DR PIR; S70524; S70524.
 DR HSSP; P32455; 1DG3.
 DR GeneW; HGNC:183; GBP2.
 DR H-InvDB; HIX000764; -.
 DR MM; 600412; -.
 DR GO; GO:0005525; F GTP binding; TAS.
 DR GO; GO:0006935; Immune response; TAS.
 DR InterPro; IPR00319; GBP.
 DR Pfam; PF02263; GBP; 1.

DR Pfam; PF02841; GBP C; 1.
 KW GTP-binding; Interferon induction; Lipoprotein; Multigene family;
 KW Prenylation.
 FT NP BIND 45 52 GTP (By similarity).
 FT NP BIND 97 101 GTP (By similarity).
 FT LIPID 588 588 S-geranylgeranyl cysteine (By similarity).
 FT CONFLICT 303 303 S -> G (In Ref. 3).
 SQ SEQUENCE 591 AA; 67183 MW; E090509EE8FC8A8 CRC64;
 Query Match 62.3%; Score 1897; DB 1; Length 591;
 Best Local Similarity 63.5%; Pred. No. 4.6-88;
 Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

Qy 1 MALEHIMSDPMLCLENFNEOLKVNQEAEILEILSTQPVVVVAYIVGLYRTGKSYLMNLLAG 60
 Db 1 MAPEINDEGPMSLIDNTKQQLVNPNEALKLISATQPVVVVAYIVGLYRTGKSYLMNLLAG 60

Qy 61 KNGKGFSVASTVOSHTKGIVIWCYPHPWPNHFLVLLDTEGHGDVEXADNKNDIQIFAL 120
 Db 61 KNGKGFSLGTVSTVSKHKGIVIWCYPHPWPNHFLVLLDTEGHGDVEXADNKNDIQIFAL 120

Qy 121 LLSSTFVNTVANKIDQAGIDLHNNTPLTDLKKARNSPDLDRVEDPADSASPFPDLWTL 180
 Db 121 LLSSTFVNTVNSMGTINQAMDQLHYTELDRIKANSPGNNSYDSDAFVSTFPATFWTL 180

Qy 181 RDFCLGLEIDGQTLVTPBEYLENSLRPKQGSQDORVQNFNLPRLCIQLKEFPKCKCFIFDLP 240
 Db 181 RDTTLTELEVDPGTTADYDLESLQSLRKGTDKXSKSNDPRLCKFPPKACCFVFDMPA 240

Qy 241 HQKKLAQLETLFDDLEPEFVQVTTFCSYIIFSHSMKTKLPGGIMYNGSRLKNLVITYVN 300
 Db 241 PKCYLAHLEQQLKEEELNPFDIQCVAEFSYLSHNVNTLQGAYVPRLSPRSVLYVN 300

Qy 301 AISSGDPICENAVLAAQRENNSAVOKAIAHYDQMGQKVLPMETIQLELDLHRTSER 360
 Db 301 AISSGDPICMENAVLAAQIENSAAVEKAIAHYEQQGQKVLPETIQLELDLHRSER 360

Qy 361 EAIEFVMKNSFKDQSFQKELETTLDQAKNDICKRNLLEASSDYCSAHLKDIFGPLEAV 420
 Db 361 EAIEFVMKNSFKDQDQMFQKLGAQLEARRDFCKQNSKASSDCMALLQDFGPLEEDV 420

Qy 421 KQGJYSKPGGHNLFIQKTBELFAYKTYREPRKGQIAEVTQKYLKSKEVSHTLQTDQAL 480
 Db 421 KQGTSKPGGQYRFTQKLQELKNNYYQPKGQIAEVTQKYLKSKEVSHTLQTDQALQTDQSL 480

Qy 481 TETEKKKEAQKAEEAKAERLAAIQRQNOMQMERLHQEQVRO --- MEIAKQNW 536
 DR :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 DB 481 SEREKAEVERLKAESAEEAKCWMLEIQLKNNEMMEKEKSYQEHVQLTERMERDRQL 540

Qy 537 LAEQQ --- KHOEQQMVFNFISPLPVTNRVSSGREGAERSCSQQGVW 585
 DR :|||: :|||: :|||: :|||: :|||: :|||:
 DB 541 MAEQEKTIAKLQKQE --- RLKEKGFENESKR --- LQDQW 575

RESULT 10

Q6GPH0 PRELIMINARY; PRT; 591 AA.

ID Q6GPH0
 AC Q6GPH0;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Glycan-like binding protein 2, interferon-inducible.
 GN Name=GBP2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR TISSUE=Skin.

Qy	481 TETEKKKKCAQVKAEEKAQPLAAIQRNQOMMQRERLHQEVHQ---MEIAKQNW 536	FT	LIPID	586	586	S-geranylgeranyl cysteine (partial).
DB	449 TEKEKEIVETCVAEASADASAKAEEEMQKIQMMEKEKTSQEVHQVQLEKMERBQL 508	SQ	SEQUENCE	589 AA;	67711 MW;	1A2947DF443640CE CRC64;
Qy	537 LAEQQ----KMQEQ 546	Query	Match	58.0%	Score 1765.5;	DB 1;
DB	509 LEEQEKTTSKLOEQ 523	Best Local	Similarity	61.7%	Pred. No. 2e-81;	
		Matches	343;	Conservative	95;	Mismatches 109;
					Indels 9;	Gaps 2;
RESULT 12						
GPL_MOUSE	GPL_MOUSE	STANDARD;	PRT;	589 AA.		
ID	AC_001514;	AC	001514;			
DT	01-JUL-1993	(Rel. 26, Created)				
DT	01-JUL-1993	(Rel. 26, Last sequence update)				
DT	05-JUL-2004	(Rel. 44, Last annotation update)				
DE	Interferon- α -induced guanylate-binding protein 1 (GDPBP-1) (mGDPBP-1)					
DE	(Guanine nucleotide-binding protein 1) (mGDPBP-1) (Interferon- γ inducible protein MAG-1).					
GN	Name: Synonyms=Gbp-1, Mag-1, Myal1;					
OS	Mus musculus (Mouse);					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX						
RN	NCBI_TaxID=10090;					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE:92031752; PubMed=1753106;					
RA	Wynn T.A., Niclou C.M., Paulnock D.M.;					
RT	"Identification and characterization of a new gene family induced during macrophage activation."					
RR	J. Immunol. 147:4384-4392 (1991).					
RN	SEQUENCE FROM N.A.					
RX	MEDLINE:910312675; PubMed=1715024;					
RA	Cheng Y.-S. E., Patterson C.E., Staeheli P.;					
RT	"Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif and bind GMP in addition to GDP and GTP.";					
RJ	RJ. Mol. Cell. Biol. 11:4717-4725 (1991).					
RN	ISOPRENOID.					
RX	MEDLINE:20346950; PubMed=10888661;					
RA	Stickney J.T., Buss J.E.;					
RT	"Murine guanylate-binding protein: incomplete geranylgeranyl isoprenoid modification of an interferon-gamma-inducible guanosine triphosphate-binding protein."					
RJ	RJ. Mol. Biol. Cell 11:219-220 (2000).					
CC	-1- FUNCTION: Binds GTP, GDP and GMP.					
CC	-1- INDUCTION: By interferon gamma during macrophage activation.					
CC	-1- PTM: Preylation of mouse GBP1 is incomplete. It persistently exists in the cell as a mixture of C20-modified and (more predominantly) nonmodified form.					
CC	-1- SIMILARITY: Belongs to the GBP family.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	EMBL; M63961; AAA9486.1;					
DR	M55544; AAA7666.1;					
DR	PIR; A46459; A46459.					
DR	HSSP; P2455; 1DG3.					
DR	M63961; 95566; GBP1.					
DR	InterPro; IPR00319;					
DR	Pfam; PF02263; GBP_1.					
DR	Pfam; PF02841; GBP_C_1.					
KW	GP-binding; Interferon induction; Lipoprotein; Multigene family;					
FT	NP_BIND 45 52 GTP (By Similarity);					
FT	NP_BIND 97 101 GTP (By Similarity);					

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DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE	(Guanine nucleotide-binding protein 2) (p67).
GN	Name=Gbp2;
GN	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC	[1]
OX	RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND ISOPRENOID.
OX	MEDLINE=1998287; PubMed=48370; DOI=10.1016/S0898-4478(94)90284-4;
RX	Asundi V.K., Stahl R.C., Showalter L., Conner K.J., Carey D.J.; Carey D.J.;
RX	"Molecular cloning and characterization of an isoprenylated 67 kDa protein.",
RT	Biochim. Biophys. Acta 1217:257-265(1994).
RT	CC -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
RL	CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC	CC -!- INDUCTION: By interferon gamma.
CC	CC -!- SIMILARITY: Belongs to the GBP family.
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CC	EMBL: M80367; AAA19309.1; ALT_INIT.
DR	DR: S43506; S43506.
DR	HSSP; P32455; 1DG3.
DR	InterPro; IPR003191; GBP.
DR	PFam; PF02263; GBP_1.
DR	PFam; PF02841; GBP_C; 1.
DR	GTB-binding; Interferon induction; Lipoprotein; Multigene family; Prey-binding; Interferon induction; Lipoprotein; Multigene family; Prey-binding.
FT	NP_BIND 45 52 GTP (By similarity).
FT	NP_BIND 97 101 GTP (By similarity).
FT	LIPID 586 586 S-geranylgeranyl cysteine.
SQ	SEQUENCE 589 AA; 67109 MW; 5E32B79102C2D97F CRC64;
DR	PIR: S43506; S43506.
DR	InterPro; IPR003191; GBP.
DR	PFam; PF02263; GBP_1.
DR	GTB-binding; Interferon induction; Lipoprotein; Multigene family; Prey-binding; Interferon induction; Lipoprotein; Multigene family; Prey-binding.
DR	NP_BIND 45 52 GTP (By similarity).
DR	LIPID 586 586 S-geranylgeranyl cysteine.
DR	SEQUENCE 589 AA; 67109 MW; 5E32B79102C2D97F CRC64;
Query Match	57 88% Score 1757.5; DB 1; Length 589;
Best Local Similarity	63.3%; Pred. No. 5.2e-81;
Matches	346; Conservative 82; Mismatches 116; Indels 3; Gaps 1
Qy	1 MALETHMSPDMCLTENNEQNLQVNGEAEALEILSATIQPVVYVAIVGLYRTGKSYLMMNKLQAG 60
Db	1 MASEHMLQPMCLTENNEQNLQVNGEAEALEILSATIQPVVYVAIVGLYRTGKSYLMMNKLQAG 60
Qy	61 KNKGGSVAVTQSHFKGIWTCVPBPWNPAHTLVLLDTEGLDVEKADRNNDIQIFALAL 120
Db	61 KRTGSLGSGTQSHFKGIWTCVPBPWNPAHTLVLLDTEGLDVEKGDQNNDCWIFALAV 120
Qy	121 LLSSSTFVYNTVNKIDQGAIDLHNTVTELTDILKARNSPDLDVEPDADSASFFPDLYWTL 180
Db	121 LLSSSTFVYNSMGTTINQMQHLYTELTLSIKSSPDSGIDASANFVGFPTFWAL 180
Qy	181 RDFCIGLEIDGQLYTPDEVYLENSLAPKQGSDQRVQNFNLPRLCIQKFPKKKCFIDLP 240
Db	181 RDFSFLGKLEIDGQLYTPDEVYLENSLAPKQGSDQRVQNFNLPRLCIQKFPKKKCFIDLP 240
Qy	241 HQKQKLAQLETLPLPDELEPFPQVQTBFCSMTPKSHMTKLPGGIIMVNGSLKLNLLVTVN 300
Db	241 LRKQKCLKLETIGEEBLICSEVEQVLEFTSYLSYSAVKTLSGGITVNGPRLKSLVQTYVG 300
Qy	301 AISSGDLPLCPTENAVIALAQPENSAAVOKAIAHYDQOMGOKVQLPMTLOELIDLHRTSER 360
Db	301 AISSSLPNEASVITLAQIENSAAVOKAIAHYDQOMGOKVQLPMTLOELIDLHRTSER 360
Qy	361 EAIEFVMKNSFKDVSFQKELETLDAKONDICKRNLEASSDYCSSLKDIFGPLFEAV 420
Db	361 EAIEFPLKNSFKDVSFQKELETLDAKONDICKRNLEASSDYCSSLKDIFGPLFEAV 420

Qy	421	KQGITSKPGHNLFIQKTEELAKKYRERPKGQIAEFLQKYLKSKEVSVAHILQTDQAL	480	Schein A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
Db	421	KQGITSKPGHNLFIQKTEELAKKYRERPKGQIAEFLQKYLKSKEVSVAHILQTDQAL	480	RT RT and mouse cDNA sequences"; RT
Qy	481	TEPEKCKKQEAQVKAEEKAQBLAAQORNEQMQERERLHQEVQRMETAKONWLAEQ	540	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Db	481	TEPEKCKKQEAQVKAEEKAQBLAAQORNEQMQERERLHQEVQRMETAKONWLAEQ	537	-1- INDUCTION: Binds GTP, GDP and GMP (By similarity). CC -1- SIMULATION: By interferon gamma during macrophage activation.
Qy	541	QKMQEQQQ	547	CC -1- SIMILARITY: Belongs to the GBP family.
Db	538	KKLJEEQ	544	CC
RESULT 15				
GPBP2_MOUSE				
ID	GPBP2_MOUSE	STANDARD; PRT;	589 AA.	CC
AC	Q920E6; Q8C1C6; Q921NP; Q9R110;			CC
DT	29-MAR-2004 (Rel. 43, Created)			CC
DT	29-MAR-2004 (Rel. 43, Last sequence update)			CC
DT	05-JUL-2004 (Rel. 44, Last annotation update)			CC
DE	Interferon-induced quanylate-binding protein 2 (GTP-binding protein 2) (Guanine nucleotide-binding protein 2) (mGBP2-2).			CC
DE	(Guanine nucleotide-binding protein 2) (mGBP2-2).			CC
GN	Name=GPBP2;			CC
OS	Mus musculus (Mouse).			CC
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			CC
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			CC
OX	NCBI TaxID=10090;			CC
RN				KW
RN	SEQUENCE FROM N.A.			Prenylation.
RC	SEQUENCE FROM 57BL/6;			FT
RX	MEDLINE=99077537; PubMed=98627071;			NP-BIND
RA	Klethlein L., Klamp T., Ozbek A., Schaub A., Futterer A.,			FT
RA	Pfeffer K., Howard J.C.,			LIPID
RA	"Two families of GTPases dominate the complex cellular response to			FT
RT	IFN-gamma.";			CONFLICT
RL	J. Immunol. 161:6715-6723 (1998).			FT
[1]				CONFLICT
RN	SEQUENCE FROM N.A. AND ISOPRENOID.			FT
RC	SEQUENCE FROM 57BL/6; TISSUE=Bone marrow;			SEQUENCE
RX	MEDLINE=99074031; PubMed=9583320;			589 AA;
RA	Buss J.E., McErcher S.R., Jenkins N.A., Copeland N.G.,			66739 MW;
RA	Keiner G.S., Asundi V.K., Zhang X., Maki R.A.;			8E68B0A3B05F3AE3 CRC64;
RT	"Murine GBP-2: a new IFN-gamma-induced member of the GBP family of			
RT	GTPases isolated from macrophages.";			
RL	J. Interferon Cytokine Res. 18:977-985 (1998).			
[2]				
RN	SEQUENCE FROM N.A.			Query
RC	SEQUENCE FROM 57BL/6; TISSUE=Kidney;			Match
RX	MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099113938;			Best Local Similarity
RA	Anderson S.L., Carton J.M., Buetow K.H., Rubin B.Y.,			62.8%;
RT	"Genomic organization and chromosomal localization of a new member of			Pred. No. 1-2e-80;
RT	the murine interferon-induced guanylate-binding protein family.";			Matches 349;
RL	J. Interferon Cytokine Res. 19:487-494 (1999).			Mismatches 114;
[3]				Indels 9;
RN	SEQUENCE FROM N.A.			Gaps 2;
RC	SEQUENCE FROM 57BL/6; TISSUE=Kidney;			DB
RX	MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099113938;			1
RA	Anderson S.L., Carton J.M., Buetow K.H., Rubin B.Y.,			MALEIMIDESPMCLLNFNEQALEILSAAITQPVVVAIVGLYRTGKSYLMNKL
RT	"Genomic organization and chromosomal localization of a new member of			60
RT	the murine interferon-induced guanylate-binding protein family.";			1 MASEIMESPMCLLNFNEQALEILSAAITQPVVVAIVGLYRTGKSYLMNKL
RL	J. Interferon Cytokine Res. 18:977-985 (1998).			60
[4]				61 KNGKFSVASTVQSHTKGIWCVHPWPWPNH1VLLTEGLDYEKADKNNDIQIFAL
RN	SEQUENCE FROM N.A.			120
RC	SEQUENCE FROM 57BL/6; TISSUE=Kidney;			61 KRTFSLGSLSTVQSHTKGIWCVHPWPWPNH1VLLTEGLDYEKADKNNDIQIFAL
RX	MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099113938;			121
RA	Anderson S.L., Carton J.M., Buetow K.H., Rubin B.Y.,			LISSSTFVYNTVVKIDQAGIDLHNNTTELDLKARNSPFLDVEPDADASFPFDLWTL
RT	"Genomic organization and chromosomal localization of a new member of			180
RT	the murine interferon-induced guanylate-binding protein family.";			121 LISSSTFVYNTVVKIDQAGIDLHNNTTELDLKARNSPFLDVEPDADASFPFDLWTL
RL	J. Interferon Cytokine Res. 19:487-494 (1999).			181 RDFGFLGLIDGQLVTPDEYLENSLRPKQGSDQVRQNFMLPRCLIQKPFKKCFIFDLP
[5]				240
RN	SEQUENCE FROM N.A.			181 RDFSLELEVNGKPVTSDEYLEHSLTLKQGADKTKTSFNEPRLCIRKEPKRKCIFIDRPA
RC	SEQUENCE FROM 57BL/6; TISSUE=Kidney;			240
RX	MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099113938;			241 HQKQLAQBLTPDDELEPFVQOTTEFCSYIISHSMTXPLPGGIMYNGSRLKNLVLTYN
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			300
RA	Klauschuk R.D., Collins F.S., Wagner L., Shnenben C.M., Schuler G.D.,			241 QRQLSKLETLRBELLGEFVEQAFTSYIISLSVQYTVG
RA	Aldschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Blat N.K.,			300
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			301 AISSGDLPCITENAVLAQRENSAVAKAIHYDQOMCQKVLPMETIQLEDLHRTSER
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			301 AISNGSLPCMEASVTLAQIENSAVAKAITHIEQNMQKIQNPTETIQLEDLHRTSER
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,			360
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			361 EAIEVEMKNSFKDQDOSFOKELETLDAKQNDICKRNLEASSDPSYCSAIIKDFGPLEFAY
RA	Raha S., Loquellano N.J., Peters G.J., Abramson R.D., Mullany S.J.,			420
RA	Boja S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			361 EAIEVEMKNSFKDQDOSFOKELETLDAKQNDICKRNLEASSDPSYCSAIIKDFGPLEFAY
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			420
RA	Villalobos D.K., Munnay D.M., Sodergren E.J., Lu X., Gibbs R.A.,			421 KQGTYSKGGHNLFIQKTBELAKKYRERPKGQIAEEVLTQYTKSKESVSHAIQTPQAL
RA	Fahay J., Helton B., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			480
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			421 KLGPFSKGGYLYLFLQMQELEKYNQAPGKGIQAEAMLNQYEDSKADYVETLQTDQSL
RA	Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,			480
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,			481 TEETKKKEAQVRAEAKAQAQLAATORNEOMQERLHQEVQV ---QMEIAKONW
RA				536

Db 481 TEAAKEVEEERTKAAEAANRELEKKQKSFELMMQQKERSYQBTVKLTERKMDEQQL 540
Qy 537 LAEQQ----RNQEQQ 547
Db 541 LAEQENIIAAKLRQE 556

Search completed: May 20, 2005, 13:31:58
Job time : 183 secs

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